#### STIC Biotech/ChemLib

77769

Fr m: Sent: Ford, Vanessa

Thursday, October 10, 2002 5:38 PM

To: STIC-Biotech/ChemLib

Subject:

In re: 09543407 Sequence seardh

Please search SEQ ID NO: 5 and please run an oligmer search on SEQ ID NO: 5.

I also need interference searches run.

Thanks!

Vanessa L. Ford

Biotechnology Patent Examiner

Office: CM1 8B13 Mailbox: CM1 8E12 Phone: 703.308.4735

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_\_Phone: \_\_\_\_\_\_
Location: \_\_\_\_\_
Date Picked Up: \_\_\_\_\_\_
Date Completed; \_\_\_\_\_\_
Searcher Prep/Review: \_\_\_\_\_\_
Clerical: \_\_\_\_\_\_
Online time:

TYPE OF SEARCH:

NA Sequences:

AA Sequences:

Structures:

Bibliographic:

Litigation:

Full text:

Patent Family:

Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

### THIS PAGE BLANK (USPTE

```
A_Geneseq_032802:*

1: /SIDSI/gcgdata/g
2: /SIDSI/gcgdata/g
3: /SIDSI/gcgdata/
4: /SIDSI/gcgdata/
5: /SIDSI/gcgdat
5: /SIDSI/gcgdat
7: /SIDSI/gcgdat
7: /SIDSI/gcgdat
8: /SIDSI/gcgdat
9: /SIDSI/gcgdat
10: /SIDSI/gcgd
10: /SIDSI/gcgd
11: /SIDSI/gcgd
11: /SIDSI/gcgd
12: /SIDSI/gcgd
13: /SIDSI/gcgd
14: /SIDSI/gcgd
15: /SIDSI/gcgd
16: /SIDSI/gcgd
16: /SIDSI/gcgd
17: /SIDSI/gcgd
18: /SIDSI/gcgd
18: /SIDSI/gcgd
19: /SIDSI/gcgd
19: /SIDSI/gcgd
19: /SIDSI/gcgd
19: /SIDSI/gcgd
19: /SIDSI/gcgd
10: /S
                                                                                                                                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB seq
                                                                                                                                                                                                                                                                                                                                                                         Score
      151
151
127
122
118
113
113
112
112
110
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-543-407-5
151
1 MKLLKVAAFAAIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         October 11, 2002, 21:14:28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1993 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1993 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1993 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1995 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1997 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1998 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990 DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990 DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyright
                                                                                                                                                                                                                                                                                                                                                                     Length DB
      151
151
151
151
151
151
120
120
151
151
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version (c) 1993 - 2002
      115
21
21
21
21
21
21
21
21
21
                                                                                                                                                                                                                                                                                                                                                                     IJ
                               AAR74625
AAB36341
AAB36346
AAW23570
AAB36347
AAB36347
AAW23561
AAW23569
AAB36355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Search time 33 Seconds (without alignments) 508.247 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1.3
Compugen Ltd
AgfA::PT3#2 amino
AgfA::PT3#3 amino
AgfA sequence. Sa
Salmonella enterit
AgfA::PT3#7 amino
AgfA::PT3#10 amino
AgfA::PT3#4 amino
                                                                                                                                                                                                          AgfA sequence. Sa
Salmonella enterit
AgfA::PT3#1 amino
Salmonella enterit
                                                                                                                                                                                                                                                                                                                                                  Description
```

normal u	AAY59838	20	257	4.6	7	5
	AAY74001	20	257	4.6	7	4
Human transcriptio	ABB50247	22	233	4.6	7	ω
	AAG91579	22	206	4.6	7	2
Novel human diagno	ABG25515	22	204	4.6	7	Ξ
	AAU01009	22	145	٠	7	0
-	AAW38495	19	80	4.6	7	9
an secretec	AAG02138	21	64	•	7	8
Esch	AAR52663	15	122	•	9	37
coli	AAB36330	21	22	6.0	9	6
	AAB36333	21	19	6.6	10	5
coli	AAB36343	21	151		11	34
n bind	AAR52664	15	142		11	ພ
	AAB36336	21	19		19	2
Salmonella enterit	AAB36328	21	19		19	31
	AAB36323	21	19		19	õ
	AAB36339	21	22	14.6	22	9
	AAB36337	21	22	14.6	22	8
_	AAB36327	21	22	14.6	22	27
	AAB36325	21	22	14.6	22	8
Salmonella enterit	AAB36322	21	22	14.6	22	ß
	AAB36320	21	22		22	24
_	AAB36318	21	22	14.6	22	ü
D	AAB36340	21	23		23	2
Ø	AAB36338	21	23		23	21
a	AAB36326	21	23		23	õ
	AAB36324	21	23		23	9
_	AAB36321	21	23	•	23	8
enteri	AAB36319	21	23		23	7
nella e	31	21	45	29.8	45	5
::PT3#5	AAB36350	21	. 151	•	70	5
::PT3#8	AAB36353	21	151	51.7	78	4
::PT3#9	AAB36354	21	151	53.0	80	ω
AgfA::PT3#6 amino	AAB36351	21	151	57.6	87	2

## ALIGNMENTS

```
RESULT 1
AAR74625
Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                         N-PSDB;
                                                                    Clouthier SC,
                                                                                                                                                                                                         Salmonella; AgfA;
                                          WPI; 1994-358275/44.
N-PSDB; AAQ87467.
                                                                                    (KING/) KING J. (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                 26-APR-1993;
                                                                                                                                   26-APR-1994;
                                                                                                                                                                      W09425598-A.
                                                                                                                                                                                         Salmonella.
                                                                                                                                                                                                                            AgfA sequence.
                                                                                                                                                                                                                                              26-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                 AAR74625;
                                                                                                                                                                                                                                                                                 AAR74625 standard; Protein; 151
                                                                                                                                                     10-NOV-1994.
                                                                     Collinson SK,
                                                                                                                 93US-0054452
                                                                                                                                   94WO-IB00207.
                                                                                                                                                                                                            vaccine
                                                                   Doran JL, Kay
                                                                                                                                                                                                                                                                                  Ą
```

AAB36349

```
SX CCCCXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
AAB36341
Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig7B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36341 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36341;
           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segmence which encodes a foreign epitope or antigen. Also described are: segmence which encodes a foreign epitope or antigen. Also described are: segmence which encodes a foreign epitope or antigen. Also described are: segment of thin aggregative fimbriae (SEF17/MAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia comprising recombinant agreement agraes and agfAr homologue fabrians in subunits, respectively: (2) of the homologues species; (3) directing recombinant gene into the chromosome of the homologues species; (3) directing recombination of a recombinant gene:
                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
                                                                                                                                                                     Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                         White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
   back into the chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGUHNGGGUSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATAÑQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151;
                                                                                                                                                                                                                                                                              2000-672631/65
DB; AAC64617.
                                                                                                                                                                                                                                                                                                                        AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                             Collison
        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AÄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 151
Pred. No.
                                                                                                                                                                                                                                                                                                                                SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
         homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                              Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3e-144;
         species,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
```

```
comprising separating an amino acid polymer comprising a recombinant of AgfA protein containing a replacement segment or segments of foreign comprising sequence or sequences grown on a Salmoneila, E. coli or comprising a recombinant of containing a replacement segment or segments of foreign comprising a recombinant of foreign containing a replacement segment or segments of foreign containing an introducing the composition of the expression of recombinant AgfA protein which is useful composition an immune response in an animal. In a fimbrial presentation composition the heterologous antigens are presented in high numbers (up to composition to the hybrid fimbrial protein possesses both the communogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong communogenic, which may be important for directing an immune response communogens, which may be important for directing an immune response communogens, which may be important for directing an immune response communogens, which may be important for directing an immune response communogens, which may be important for directing an immune response community to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
AAB36346
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copy of that gene; and (4) eliciting an immune response in an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36346 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#1 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                        WO200060102-A2
                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                             WPI; 2000-672631/65
N-PSDB; AAC64622.
                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                         12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                              White AP,
                                                                                                                                                                          (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITOSGYGNGADYGOGADNSTIELTONGFRNNATIDQWNAKNSDITYGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; ilarity 100.0%; Conservative
                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                            99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                      response;
                                                                                                                                                                                                                                                                                                                                                                                                                    chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                 Collison
                                                                                                                                                                                                                                                                                                                                                                                                      immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 151; DB 21
Pred. No. 3e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                    SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                    Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:12.
                                                                                                                                                      WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ç,
```

0,

Recombinant agfA gene having a segment replaced by a foreign sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response

response

in animal

DNA

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful CC useful for the expression of recombinant AgfA protein which is useful CC for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 coples/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong clauminogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and cliexpensive to purify in large amount. The present sequence is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmontala, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
26-APR-1994;
                                      26-APR-1993;
                                                                             03-JUN-1997
                                                                                                                  US5635617-A.
                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                     Salmonella enteritidis
                                                                                                                                                                                                                                                                          Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                              Salmonella enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                   29-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW23570 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 135; 139pp; English.
94US-0233788
                                      9305-0054452
                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                         /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 127; DB 21; Le
%; Pred. No. 4.8e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
```

```
RESULT 5
AAB36347
ID AAB3
Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\ext{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\exitinx{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\exititt{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\exitin}$}}\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 9% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can be used to provide proteins and antibodies which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family
                          White AP,
                                                                                                                                        05-APR-1999;
                                                                                                                                                                                              05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#2 amino acid sequence SEQ ID NO:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36347 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virtually all other microbial organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA INNOVATION & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1993;
                                                                             (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response;
                       Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                        99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0054452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.8%; Score 122; DB 18; 100.0%; Pred. No. 5.3e-115;
                          Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                          SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
```

```
cc directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant cc comprising separating an amino acid polymer comprising a recombinant cc amino acid sequence or sequence syrown on a Salmonella, E. coli or cannot acid sequence or sequence grown on a Salmonella, E. coli or complymer into the animal in conjunction with a carrier or diluent. (I) is conjunct into the expression of recombinant AgfA protein which is useful comparising an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is conjunction with a carrier dimbrial protein possesses both the carrier dimbrial protein possesses both the carrier dimbrial subunit proteins are usually strong conjunction. The present of dimension in the carrier dimbrial protein possesses between the carrier dimbrial proteins are easy and conjunction with a carrier dimbrial present sequence is given in the carrier d
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
AAB36348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-672631/65.
N-PSDB; AAC64623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Agfa, CsgA and Agfa homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                    AgfA::PT3#3 amino acid sequence SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36348 standard; Protein; 151
                                                                                                                                                               Salmonella enteritidis
                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                    26-FEB-2001
                      12-OCT-2000
                                                                                                                                           Escherichia coli
                                                                                                                                                                                                               vaccine;
                                                                    WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118;
                                                                                                                                                                                                                  immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.1%;
                                                                                                                                                                                                                       immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                   fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
```

RESULT 7 AAR62761

AAR62761 standard; Protein; 120

AAR62761;

OS XXX

AgfA sequence 26-JUN-1995

(first entry)

Salmonella; AgfA; vaccine

Salmonella enteritis 27655-3b

Qy

Matches Query Match Best Local :

113;

Conservative

0;

Mismatches

Indels.

0;

Gaps

0

74.8%;

Local Similarity

Qy В

NNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMYRQVGFGNNATANQY

NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY

151

SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR 98 SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR 98

```
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                   copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or enterplacement containing the Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is polymer into the expression of recombinant AgfA protein which is useful useful for the expression of recombinant AgfA protein which is useful useful for immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC64624
                                                                                                                                                                                                           vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                       immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                                                                               the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                             151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collison
Score 113; DB 21;
Pred. No. 6.3e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Кау
                                              Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal
```

```
δ
                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the Salmonella enteritis 27655-3b TnphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans.
                          Clouthier SC,
                                                               26-APR-1994;
26-APR-1993;
                                                                                           26-APR-1993;
                                                                                                              03-JUN-1997
                                                                                                                                                 Salmonella enteritidis
                                                                                                                                                                   Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                                                                                                           29-SEP-1997
                                                                                                                                                                                                                            AAW23569
                                                                                                                                                                                                                                             AAW23569 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig7A; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9425598-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-358275/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KING/) KING J.
(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1994;
                                             (UYVI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1994
                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                         22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITOSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                  ۳
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
        1997-309886/28
                                                                                                                                                                                                                                                                                          VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                      112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ73066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an immune response to Salmonella -
                                                                                                                                                                                                                                                                                                                                                                                                           120 AA;
                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                            VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                        (first entry)
                          Collinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collinson SK,
                                                               94US-0233788
93US-0054452
                                                                                          9305-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-IB00207
                                                                                                                                                                                                                                                                                                                                                                              74.28;
                                                                                                                                                                                     27655-3b TnphoA mutant agfA fragment
                          SK,
                                                                                                                                                                                                                                              120

 Mismatches

                                                                                                                                                                                                                                                                                                                                                                             Score 112; DB 15;
Pred. No. 5.2e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doran JL,
                         Doran JL,
                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ella - using
or compsns.
                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay ww;
                                                                                                                                                                                                                                                                                                                                                                                      Length 120;
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             attenuated contg.
                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                     0
```

```
RESULT 9
AAB36352
FF FF XX XX OOO
                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b InphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for
                                                                                                                                                    White AP,
                                                                                                                                                                                                     05-APR-1999;
                                                                                                                                                                                                                          05-APR-2000;
                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36352 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family
                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                 12-OCT-2000
                                                                                                                                                                                                                                                                         WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#7 amino acid sequence SEQ
                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
112; Conserv
                                                                                                                  AAC64628
                                                                                                                                                                                                                                                                                                                                              immune
                                                                                                                                                   Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                           2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                   99US-0127888
                                                                                                                                                                                                                                                                                                                                              response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.28;
                                                                                                                                                    Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                              immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 112; DB 18;
Pred. No. 5.2e-105;
                                                                                                                                                    SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                    Kay
                                                                                                                                                                                                                                                                                                                                                                                  IJ
                                                                                                                                                                                                                                                                                                                                                                                  NO:24
                                                                                                                                                    ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                   in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

The present invention describes a recombinant agfA gene segment of the gene has been replaced by a segment of a

where a foreign DNA

Disclosure;

Page 138; 139pp; English.

immune response in animal

```
copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant of comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or canterbacteriaceae host cell, from the host cell and introducing the Enterobacteriaceae host cell, from the host cell and introducing the conjumer into the animal in conjunction with a carrier or diluent. (I) is conjumer into the expression of recombinant Agfa protein which is useful cuseful for the expression of recombinant animal. In a fambrial presentation conjunction which a carrier or diluent. (I) is conjunction which is useful conjunction with a carrier or diluent. (I) is conjuncted to the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fambrin protein possesses both the carrier fambrial subunit proteins are usually strong conjunction, which may be important for directing an immune response capalist the inserted epitope, and hybrid fimbriae are easy and conjunction in the present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
AAB36355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
DIT NOT THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36355 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001
                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis
                                                        WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                                                                                                                                     05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
Recombinant agfA gene having
                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                       Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                           99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%;
                                                                                                                                                             Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 110; DB 21; pred. No. 6.7e-103;
            a segment replaced by a foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                SK,
                                                                                                                                                                Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

Salmonella enteritidis Escherichia coli

05-APR-2000; 2000WO-CA00356

12-OCT-2000 WO200060102-A2 Synthetic

05-APR-1999;

9905-0127888

```
₽₽₽¥₩₩
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
AAB36349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is polymer into the expression of recombinant AgfA protein which is useful useful for the expression of recombinant AgfA protein which is useful or eliciting an immune response in an animal. In a fimbrial presentation for eliciting an antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (but to copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the present of the present incorrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and escenbiraceae for the production of fimbriae comprising recombinant hapfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36349 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                    AAB36349;
                                                                                                                                                                                                                                                                                                    AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.
02; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                    response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.5%;
                                                                                                                                                                                                                                                        immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 102;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 21;
. 7.8e-95;
                                                                                                                                                                                                                                                                                fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
```

```
RESULT 12
AAB36351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC assembly system of strains of Salmonella, Escherichia coli and C Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene composed the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant CC AgfA protein containing a replacement segment or segments of foreign CC amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful CC for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbria protein possesses both the carrier fimbrial subunit protein possesses both the CC immunogens, which may be important for directing an immune response can animal the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in the carmination of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65
                                                    Salmonella enteritidis
                                                                                                          Salmonella; agfA;
                                                                                                                                              AgfA::PT3#6 amino acid sequence SEQ ID NO:22
                                                                                                                                                                                                                                                                 AAB36351 standard; Protein; 151
                                  Escherichia coli
                                                                                          vaccine;
                                                                                                                                                                                       26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                  118
                                                                                                                                                                                                                                                                                                                                                                                    118 YGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                YGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                          ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ 117
                                                                                        immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>}</u>
                                                                                                        chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.3%; Score 94; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; 1
9.1e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                          fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
RESULT 13
AAB36354
                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                          멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTXXX
                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                            ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native cc back into the chromosome of the homologous species, replacing the native cc copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign cm anino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier or diluent. (1) is cuseful for the expression of recombinant AgfA protein which is useful cor eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrial protein possesses both the carrier fimbrial subunit proteins are usually strong the immunogenes which may be imported for the subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
N-PSDB; AAC64627.
                                                                            AAB36354;
                                                                                                                AAB36354 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 137; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1999;
                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                      exemplification of the present invention
                                                                                                                                                                                                             SDARKSETTITOSGYGNGADVGQGADN 87
                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADN
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                     57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                       Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
. 1e-79;
                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is given
                                                                                                                                                                                                                                                                                                                                                                Gaps
```

in

0

AgfA::PT3#9 amino acid sequence SEQ ID NO:28

26-FEB-2001

(first entry)

```
cc segment of the gene has been replaced by a segment of a foreign DNA cc sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended cc assembly system of strains of Salmonella, Escherichia coll and cd affa, CsgA and AgfA-homologue fimbria subunits, respectively: (2) cc AgfA, CsgA and AgfA-homologue fimbria subunits, respectively: (3) cc AgfA, CsgA and AgfA-homologue fimbria subunits, respectively: (3) cc AgfA, CsgA and AgfA-homologue fimbria comprising recombinant gene cc back into the chromosome of the homologous species: (3) directing recombination of a recombination of firm a replacement of segments of foreign of a replacement segment or segments of foreign of a recombination of recombination with a carrier or diluent. (1) is of the presentation of recombination with a carrier or diluent. (1) is of the presentation of the presentation of fimbrian protein possesses both the or an endougle of the presentation of the present for directing an immune response of immunogenicity and adhesion properties relevant for an efficient live of the present segment of the present sequence is given in the beautiful of the present sequence is given in the beautiful of the present sequence is given in the pr
                                 Q
                                                                              Вр
                                                                                                                οy
B
                                                                                                                                                               Matches
                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                           Sequence
  61
                                      61 SDARKSETTITQSGYGNGAD
                                                                                                                      \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-672631/65.
DB; AAC64630.
                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  l Similarity
80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doran JL,
                                                                                                                                                                                                                                                151 AA;
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0127888
                                                                                                                                                                                    53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collison SK,
                                            80
                                                                                                                                                                   score 80; DB; pred. No. 1.2
                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW;
                                                                                                                                                                                        DB 21;
1.2e-7
                                                                                                                                                                     72;
                                                                                                                                                                                                           Length 151
                                                                                                                                                                       Indels
                                                                                                                                                                         0;
                                                                                                                                                                            Gaps
                                                                                                                                                                            0;
```

RESULT 14,

ρy

74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133

Matches Query Match Best Local

Similarity

51.7%;

Score 78; Pred. No. Mismatches

DB 21, 0, 1.2e-70; 0;

0;

0

Length 151

Conservative

0;

Sequence

151 AA;

```
AAB36353
                                                       copy of that gene; and (4) eliciting an immune response in an animal. Copy of that gene; and (4) eliciting an immune response in an animal. Copy of that gene; and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising a recombinant comprising separating a replacement segment or segments of foreign camino acid sequence or sequences grown on a Salmonella, E. coli or conjumer into the animal in conjunction with a carrier or diluent. (1) is colymer into the axpression of recombinant AgfA protein which is useful conjunction with a carrier or diluent. (1) is coliciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (1) is coliciting an immune response in an animal. In a fimbrial presentation conjunction with the heterologous antigens are presented in high numbers (up to conjunction), the hybrid fimbrin protein possesses both the conjunction properties relevant for an efficient live reactine, the carrier fimbrial subunit proteins are usually strong communogens; which may be important for directing an immune response conjunctions the inserted epitope, and hybrid fimbriae are easy and conserved in high conjunction of the present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36353 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: sequence which encodes a foreign epitope or antigen. Also described are: the control of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) the chromosome of the directing recombinant gene into the chromosome of the pomologous species; (3) directing recombination of a recom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA seguence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC64629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kay
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                            back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, cc comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or CC anino acid sequence host cell, from the host cell and introducing the cc polymer into the animal in conjunction with a carrier or diluent (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to 500,000 coples/cell), the hybrid fimbrin protein possesses both the Immunogenicity and adhesion properties relevant for an efficient live immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbrine are easy and the contribution of the contribution o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-672631/65.
N-PSDB; AAC64626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#5 amino acid sequence SEQ ID NO:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36350 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2000
                                          against the inserted epitope, and hybrid fimbriae are easy and
inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                      exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYMVROYGEGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 137; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collison
                      present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kay WW
```

```
SQ Sequence 151 AA;
```

```
Вb
               Š
                               В
                                              Ş
                                                              Query Match
Best Local S
Matches 70
142 FGNNATANOY 151
               142 FGNNATANQY 151
                              l Similarity
70; Conserv
                                                               Conservative
                                                                     46.4%; Score 70;
100.0%; Pred. No.
                                                               0;
                                                               Mismatches
                                                                     DB 21; I
. 1.5e-62;
                                                                             Length 151;
                                                              0
                                                             Gaps
                                                              0
```

Search completed: October 11, 2002, 21:19:04 Job time : 34 secs

# THIS PAGE BLANK (USPTU)

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 11, 2002, 21:18:23 ; Search time 17 Seconds (without alignments) 216.957 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-543-407-5
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                            US-08-401-136-8

US-08-850-554-8

US-08-934-846-4

US-09-238-557-4

US-09-238-557-2

US-08-190-8028-97

US-08-477-346-97
                                          US-08-477-346-97
US-08-473-089-97
US-09-053-197A-61
US-09-085-761A-66
US-08-461-990B-10
US-08-988-856B-29
US-08-910-856-6
US-09-025-769B-373
US-09-025-769B-373
US-09-026-985-53
                                                                                                                                                                                                                                                                                                                                   US-07-851-976B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                        Sequence
Sequence
                                                                                                                                                                                                                                          Sequence
Sequence
                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Appl
Sequence 57, Appl
Sequence
                                                                                                                                                                                                                                                                          Sequence
               Sequence
                              Sequence
                                            Sequence
                                                         Sequence
                                                                          Sequence
                                                                                                                      Sequence
                                                                                                                                   Sequence
                                                                                                                                                 Sequence
                                                                                                                                                                 Sequence
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                               Sequence
                                            29, Appl
6, Appli
372, App
373, Appl
53, Appl
53, Appl
53, Appl
                                                                                                                                                                97, Appl
61, Appl
66, Appl
                                                                                                                                                                                                                                                                                                        œ œ œ œ
                                                                                                                                                                                                             7, Appl
                                                                                                                                                                                                                                                       Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                          Appli
              δõ
```

4. Ст	44	43	42	41	40	39	38	37	36	35	34 .	3 3	32	31	30	29	28.
6	σ	σ	6	σ	6	σ	σ	σ	σ	6	6	σ	σ	6	σ	σ	6
4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
211	211	211	211	211	211	211	211	188	188	188	188	188	188	164	164	164	164
4	N	<u>, , , , , , , , , , , , , , , , , , , </u>	<b>—</b>	ш	_	_	_	ω	ω	N	N	N	N	w	w	2	2
US-08-907-739-16	US-08-383-619-16	US-08-899-575-34	US-08-899-575-34	US-08-387-874-16	US-08-322-730A-16	US-08-133-011-16	US-08-276-852-34	US-08-149-223A-20	US-08-458-731-20	US-08-480-150A-20	US-08-484-596A-20	US-08-484-158B-20	US-08-484-993B-20	US-08-149-223A-45	US-08-458-731-45	US-08-480-150A-45	US-08-484-596A-45
	Sequence 16, Appl	Sequence 34, Appl	Sequence 34, Appl	•	Sequence 16, Appl	-	Sequence 34, Appl	Sequence 20, Appl	•	•	•	Sequence 20, Appl	•	•	•	•	Sequence 45, Appl

ALIGNMENTS

#### ; MOLECULE TYPE: protein US-08-233-788A-59 ATTORNEY AGENT INFORMATION: NAME: King, Joshua REGISTRATION NUMBER: 35,570 REFERENCE/DOCKET NUMBER: 9200 TELEPAN: (206) 622-4900 TELEFAX: (206) 682-6031 TELEFAX: 3723836 SEEDANBERRY INFORMATION FOR SED ID NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 151 amino acids TYPE: amino acid TODOTORY: 11 near RESULT 1 US-08-233-788A-59 CITY: Seattle CITY: Seattle STATE: Washington COUNTRY: U.S.A. ZID: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS COMPUTER: PC-DOS/MS-DOS COMPUTER: PC-DOS/MS-DOS Query Match 80.8%; Best Local Similarity 100.0%; Patent No. GENERAL INFORMATION: COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,788A FILING DATE: 26-APR-1994 APPLICANT: Doran, James L. APPLICANT: Kay, William W. APPLICANT: Collinson, Karen S. APPLICANT: Clouthier, Sharon C. TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61 NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: STREET: 6300 C CITY: Seattle STATE: Washing TOPOLOGY: linear CLASSIFICATION: ADDRESSEE: 9, Application 5635617 6300 Columbia Center, 701 Fifth Avenue Seed and Berry US/08233788A Score 122; DB 1; 1, Pred. No. 1.1e-112; 920043.403C2 #1 . 25 Length 151;

Matches

Conservative

Indels

0

Gaps

0;

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-233-788A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-08-858-207A-291

Sequence 291, Application US/08858207A

: Patent No. 5348328

: GENERAL INFORMATION:
                                                                                                                                                 Š
                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                  Qy
                                                                                                                   뫄
                                                                                                                                                                                                                                                                                                                        US-08-233-788A-57
                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Appropriate No. 56356
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: line-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 26-APR CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                     61
                                                                                                                                                     82
                                                                                                                                                                                                                                                     Local Similarity
les 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                  22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                     GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                    VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                   GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: U.S.A.
98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08233788A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6300 Columbia Center,
                                                                                                                                                                                                                                                    74.2%; Score 112; DB 1; ilarity 100.0%; Pred. No. 5.9e-10 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doran, James L.
Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/233,788A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             920043.403C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.01 Fifth Avenue
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                          Length 120;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                              0;
```

```
Вb
                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-858-207A-291
                                                                                                                                                                                                                                                                           US-07-851-976B-8
                                                                                                                                                                                                                                                                                          RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                            Sequence 8,
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 09-MAY-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                   APPLICANT:
                                                                                CORRESPONDENCE ADDRESS
                                                                                                              TITLE OF INVENTION:
                                                                                                                                             APPLICANT:
                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 709 Swedeland CITY: King of Prussia
                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                     13 NAALALQ 19
                                                                                                                                                                                                                                                                                                                                                                54 NAALALQ 60
                            STATE:
         COUNTRY:
                                                        STREET:
                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RY: USA
19406-0939
                                                                                                                                                                                                                                                   5426043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 80 amino acids amino acid
94104-2675
                                          Palo Alto
                                                                                                                                                                                                                                                          Application US/07851976B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PΑ
                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: SmithKline Beecham Corporation
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stodola, Robert
VENTION: No. 6348328el Compounds
EQUENCES: 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodgson, John
Knowles, David
Nicholas, Richard
                                                        755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black, Michael
                                                                                                                                                                       Van Den Broeck, Henriette
Strozyk, Francois
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version
                                                                                                             BOORMAN, JOHANNES C.P.
VENTION: CLONING AND EXPRESSION OF ACETYL XYLAN
VENTION: ESTERASES FROM FUNGAL ORIGIN
                                                                                                                                                                                                      Visser, Jacob
                                                                                                                                                                                                                    De Graaff, Leendert H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
               USA
                                                                                                                                                            Kormelink, Felix J.M.
                                                                       Morrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/858,207A
09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 6348328e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOS
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%;
                                                                       Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291:
                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P50475
                                                                                                                                                                                                                                                                                                                                                                                                            Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
```

0;

COMPUTER READABLE FORM:

MEDIUM TYPE:

OPERATING SYSTEM: PC-DOS/MS-DOS

IBM PC compatible

oppy disk

```
RESULT 5
US-08-291-609-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-07-851-9768-8
                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1:25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,609
FILING DATE: 17-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/851,976
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MUTSBAGE 4815.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 56817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 HNGGGNS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 246152003200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: %-
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                     STREET: 755 Page )
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 4.6%; Score 7; DB Local Similarity 100.0%; Pred. No. 33 hes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 HNGGGNS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE: 19920316
                                                                                                                                                                                                                                                                                                                                        ZIP: 94104-2675
                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08291609
                                                                                                                                                                                                                                                                                                                                                                                                            755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOONMAN, JOHANNES C.P.
VENTION: CLONING AND EXPRESSION OF ACETYL XYLAN
VENTION: ESTERASES FROM FUNGAL ORIGIN
                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Visser, Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kormelink,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Den Broeck, Henriette
Strozyk, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Graaff, Leendert H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Felix J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/07/851,976B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246152003200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

밁

115 HNGGGNS 121

```
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-401-136-8
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-401-136-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-291-609-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                               Matches
                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0764
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 08-MAR-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 HNGGGNS 121
 32 HNGGGNS 38
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA .
ZIP: 20006-1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Morrison & Foerster
STREET: 2000 PENNSYLVANIA AVENUE NW, SUITE 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 HNGGGNS 38
                               Local Similarity
nes 7; Conser
                                                                                                                                                                                           TELEFAX: (202)
TELEX: 90-4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                  I: 304 amino acids
amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08401136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOONMAN, JOHANNES C.P.
VENTION: A METHOD TO ALTER THE PROPERTIES
VENTION: ACETYLATED XYLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Visser, Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-494-0792
                             4.6%; Score 7; DB llarity 100.0%; Pred. No. 33 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strozyk, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Den Broeck, Henriette C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kormelink,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Graaff, Leendert H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                            08-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%;
100.0%;
                                                                                                                                                                                                                                                                                                                                             US/08/401,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Felix J.M.
                                                                                                                                                                                                                                                                   29,959
                                                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                      4615-0032.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                             DB 1;
o. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                         Length 304;
                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF.
                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

```
RESULT 7
US-08-850-554-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-850-554-8
                                                                                                                                                                                                                                                                                                                                                                                                   US-08-934-846-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08934846. Patent No. 5882898 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 20006-18to
ZIP: 20006-18to
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: De Gra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BOONMAN, JOHANNES C.P.
TITLE OF INVENTION: A METHOD TO ALTER THE PROPERTIES OF
TITLE OF INVENTION: ACCTYLATED XYLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         APPLICANT: Pearson, S:
APPLICANT: Greenwood,
TITLE OF INVENTION: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELECUTE (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 HNGGGNS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 02-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MOTTISON & FOETSTEE NW, SUITE 5500
CITY: : Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 HNGGGNS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Murashige, Kate
REGISTRATION NUMBER: 2
                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8, Application US/08850554
o. 6010892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                 E: Dechert Price & Rhoads
4000 Bell Atlantic Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Den Broeck, Henriette
Strozyk, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Visser, Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kormelink,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Graaff, Leendert H.
                                                                                                                                                                                                                                                                        Pearson, Stewart C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887-0764
                                                                                                                                                                                            nd, Rebecca C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLATED XYLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 7; DB: 100.0%; Pred. No. 33 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 08/401,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/850,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Felix J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4615-0032.10
                                                                        1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>0</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
```

0;

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-934-846-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-238-557-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6165472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Pearson, S
APPLICANT: Greenwood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
KEGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              OPERATING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,557
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL fold NUMBER OF SEQUENCES: 4
                                                    ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 NAALALQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
COMPUTER: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 215 J.
TELEPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                     COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                         STREET: 4000 _.
CTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 NAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dickinson, To REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                   FILING DATE:
                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19103
                                                                                                                                                                                                                                                                                           19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09238557
                                                                                                                                                                                                                                                                                                                                                      3: Dechert Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/934,846
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rebecca
                                                                                                                   08/934,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GM10088
                                        GM10088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                   ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
```

```
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
RESULT 11
                                                                                                                                                         US-08-934-846-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-934-846-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5882898
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                 Matches
                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: DLCKINSON, TODD Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-994-2252
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pearson, Stapplicant: Greenwood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 NAALALQ 259
                                         253 NAALALQ 259
                                                         54 NAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 NAALALQ 60
                                                                                                                                                                                LENGTH: 418 amino
TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4000 Bell
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/934,846 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 4.6%; So Local Similarity 100.0%; P res 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 407 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                      TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-994-2222 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08934846
                                                                                                                                                                                                           418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Dechert Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                               ددی: single
linear
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOVEL folc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stewart C.
                                                                                                             4.6%; Score 7; DB 2
100.0%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rebecca C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7;
                                                                                               0;
                                                                                                                                                                                                                                                                                                               GM10088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 43;
                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                          Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                               Indels
                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                               0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-190-802A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-238-557-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-238-557-2
                                                                                                                                                                                                                                                                                        Sequence 97, Application US/08190802A Patent No. 5519003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6165472
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    TITLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca
TITLE OF INVENTION: NOVEL folo
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                        APPLICANT: Mochl APPLICANT: Ron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Dickinson, Todd Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             253 NAALALQ 259
                                                                                                                                                                                                                                                                                                                                                                                                             54 NAALALQ 60
                                                                    STATE: CA
COUNTRY: USA
ZIP: 94306-0850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4000 Bell CITY: Philadelphia STATE: PA
                                                                                                       CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U:
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/238,557
                                                                                                                                      STREET:
                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, Application US/09238557
                                                                                                                                      E: Dehlinger & Associates P.O. Box 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Dechert Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US
                                                                                                                                                                                                                                                        Mochly-Rosen, Daria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                          Dorit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVEL folc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 7; DB 4
100.0%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/934,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rebecca C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GM10088
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 418,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

Gaps

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-477-346-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-190-802A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6262023
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                            TELEFAX: (202) 887-076
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE: INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rIV, Fig. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: WD-40 -
                                                                              REFERENCE/DOCKET NUMBER: 2550-0025.20 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/49
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 IVVSGS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 IVVSGS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ropology:
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                    REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08477346
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000 Pennsylvania Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO
                   29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                   (202) 887-0763
                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WD-40 - Derived Peptides and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 6; DB
100.0%; Pred. No. 35
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/190,802A
                                                                                                                                                                                                        08/487,072
                                                                                                                                                                                                                                                                          US/08/477,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8600-0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
```

```
; INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rIV, Fig. 15 US-08-477-346-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-473-089-97
밁
                     δÃ
                                                                                                     ; INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rIV, Fig. US-08-473-089-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6342368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                  Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                  TELEFAX: (202) 887-07 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US,08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: WD-40 -
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                        TELEPHONE: (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 IVVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 IVVSGS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue,
                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,9 REFERENCE/DOCKET NUMBER:
15 IVVSGS 20
                          12 IVVSGS 17
                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                   MURASHIGE, KATE
                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08473089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ron, Dorit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mochly-Rosen, Daria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                       Conservative
                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                               (202)
                                                                                                                                                                                                                                                               2) 887-1500
887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WD-40 - Derived Peptides and Uses
                                                                    100.0%;
                                                                                  4.0%;
                                                                                                                                                                                                                                                                                                                      29,959
                                                                                                                                                                                                                                                     97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; I
                                                                                                                                                                                                                                                                                                           2550-0025.22
                                                       0; Mismatches
                                                                     Score 6;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                  Length 29;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                           0;
```

RESULT 15 US-09-053-197A-61 0,

```
Sequence 61, Application US/09053197A

PATELCANT Welher, Joel H.
APPLICANT Welher, Joel H.
APPLICANT Welher, Raymond J.
TITLE OF INVENTION: SECRETION

NUMBER OF SEQUENCES: SECRETION

NUMBER OF SEQUENCES: SECRETION

NUMBER OF SEQUENCES: SECRETION

CORRESSORDENCE ADDRESS:
ADDRESSEE: Medien 6. Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200

CITY: San Fishopy disk
MEDIUM TYPE: Ploopy disk
COMPUTER READAGE FORM:
MEDIUM TYPE: DISTANCE OF AMERICAN FILE
COMPUTER READAGE FORM:
MEDIUM TYPE: DISTANCE OF AMERICAN FILE
COMPUTER READAGE FORM:
MEDIUM TYPE: DISTANCE OF AMERICAN FILE
COMPUTER READAGE FORM:
MEDIUM TYPE: DISTANCE OF AMERICAN FILE
COMPUTER READAGE FORM:
MARCHES FORM:
```

# THIS PAGE BLANK (USPTS)

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLIGO Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-543-407-5
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           October 11, 2002, 21:17:28 : Search time 20 Seconds (without alignments) 725.474 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
        JC6039
AI0633
S70788
BD90806
HD90806
T364490
T34441
AE0940
AH2344
AE0940
AH2344
AE0940
AF1950
AB251
AB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283138
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
anthranilate phosp
prephenate dehydro
prephenate dehydro
protetical prote
hypothetical prote
translation elonga
translation elonga
                                                                                                                                                                                                                 ATP-binding protei probable ribulose-oligopeptide trans probable zinc-fing 2,3-dihydroxypheny 2,3-dihydroxypheny 2,3-dihydroxypheny 2,3-dihydroxypheny
                                                                                                                                                                                                                                                                                                                                                       hypothetical prote NADH dehydrogenase hypothetical prote conserved hypothet insulin-like growt
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical prote probable transmemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             curlin major subun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fimbrin protein ag major curlin chain
```

Оy	Qy dg	Дb	Ma Be	F; 2	A;DF	A C A A A	A; A	2 A A ;	J.R.A.	2 2 2 3 2 2 3 3	A A A A A A A A A A A A A A A A A A A	A A A A R H	л R; С	G:D	,						-	
121 NN	61 SE 61 SE	1 MK 1 MK	ery Mat st Loca tches	eywords: -20/Domai 1-151/Prc	unction: escriptic ote: fimb	olecule t esidues: ote: sequ enetics: ene: acfA	ccession: tatus: pr	itle: Pur eference	xperiment ote: the ollinson, Bacteriol	olecule t	olecule t esidues: ross-refe	itle: Sal eference ccession:	ollinson, Bacteriol	039 brin prot pecies: S ate: 31-D		44	41 42	39 40	37 37	نا دی در نا 4- اد	32	30
NNAALVNOTASDS	ARKSE	LLKVA       LLKVA	ch l Similarit 151; Conse	fimbr n: si duct:	n: ma	ype: 21-33 ence	A448 elimi	ifica numbe	autho S.K.	ype: 21-52	ype: 1-151 rence	monel numbe	S.K.	ein a almon ec-19		6	777	7 7	77	7 7	7 7	7
OTA	1 1	AF2	Laı	ia gna f:	jo:	ext pro	98 na.	T: 10	; ;	7 2	15 S: 0 DN/	1a r:	(	39 96 39		44	444	444	44	444	44.	4
SDSSV	TOSGY	VAIVVS VAIVVS	rity servat	al seq	comp	otein 303> Tracte	ÿ	on and A4489	trans trans mody,	otein 002>	OL> GB:U4	enter JC603	10uth	prec #sequ la ent		000	noo	თთσ	100	თთთ	000	σ
VMVRQV	GNGAL GNGAL	GSAL/ GSAL/	100.0% 100.0% tive	uence prot	onent fibro	d fro		chai 8; M	rain lated L.; 781.	5  	3280;	itidi 9; MU	ier, 19, 19	urson eriti ence 15: /		982 35	652 796 951	587 587 614	545	436 436	416	413
GFG	ω ω ω	64 – 6	9,00	e #	ne o	ă		ac	19 M C 2	1	z	ID	96	rei.		NNI	งผม	200	200	SNN	200	N
SVMVRQVGFGNNATANQY 151	:DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 	MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 	Score 151; DB 2; L; Pred. No. 1.3e-146; 0; Mismatches 0;	status predicted <sig> n agfA #status experimental</sig>	ative 1	(NCBIP:45		thin, a	nobsession according to the codon ACG for residue cller, K.H.; Trust, T.J.;	VIII - 25.	NID:g1184712; PIDN:AAC435	encoding	C.; Doran, J.L.; Banser,	TC6039  JC6039  JC6039  JC6039  JC6039  JC6039  JC6039  JC6039  JC6039: pr66115: A44898  JC:Accession: JC6039: pr6615: A44898	ALIGNMENTS	T19526 B33770	E97857 T08555 T08987	149357 \$65755 D84191	A46281 S46825	B83257 · T36432 E82340	H95022 B97894	861305
	WNAKNSDITVGQYGG 120                  WNAKNSDITVGQYGG 120	SIYOYGSANAALALQ 60 	Length 151; Indels 0; Gaps 0;	ntal <mat></mat>	imbriae Lissue plasminogen activator	936)		ggregative fimbriae from Salmone	; Kay, W.W.		:599.1; PID:g1184714	thin, aggregative fimbriae.	, P.A.; Kay, W.W.	idis #text_change 08-Oct-1999		hypothetical prote	cell surface antig pathogenesis-relat	<pre>tetrahydrofolylpol tetrahydrofolylpol dolichol-P-qlucose</pre>	tetrahydrofolylpol	folylpolyglutamate probable transmemb prohable gluconate	dihydrofolate synt	cycH protein - Par

121

NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

```
major curlin chain precursor [imported] - Salmonella enterica subsp. enteric
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AI0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a multiple drug resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: Arcorr
R;Parkhill, J.; Dougan, G.; James,
P.; Cronin, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                             A; Cross-references: EMBL:x90754; NID:gl147558; PIDN:CAA62282.1; PID:gl147564
A; Experimental source: strain K12, substrain W3110
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: AB0502; A; Accession: AI0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ţħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-151 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
              A;Residues: 1-151 <BLAT>
A;Residues: 1-151 <BLAT>
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1;
A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, Substrain MG1655
R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S.
Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-151 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown; translation
Mol. Microbiol.
                                                                                                                         A; Molecule type: DNA
                                                                                                                                                    A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T.; Connerton, P.; Cronin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITOSGYGNGADVGOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                         not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K.D.; Thomson, N.R.; Pickard, D.; Davis, P.; Davies, R.M.; Dowd, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 151; DB 2;
Pred. No. 1.3e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enterica subsp. enterica serovar Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skelton, J.; Stevens, K. Salmonella enterica sero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of fibronectin- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wain, J.; Churcher; White, N.; Farrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stevens, K.
                                                                                             PID:g1787279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
```

```
A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression A;Reference number: S31202; MUID:93211294
A;Accession: S31202
A;Accession: S31202
A;Cross-references: EMBL:L04979
A;Accession: S34560
A;Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: S34559
A;Accession: S34559
A;Molecule type: DNA
A;Residues: 1-133; RORDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: major component of wild-type curli; interaction between CsgA and A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia cc and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG>F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 21-42; 44-50 <OLS2
R; Olsen, A.N.; Arngvist, A.M.
                                                                                                                                                                                                                                                                                                                                             curlin major subunit CsgA [imported] - C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision C;Accession: D90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October
                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: csgA
                                                                                                                                                                                                                                                        DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90806
A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                gasawara, N.;
밁
                               2
                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                 Query Match
                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                  Local Similarity
wes 11; Conserv
 15
                                   15
                                                                                                                                        ECs1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSALAGVVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSALAGVVPQ
 SGSALAGVVPQ 25
                                   SGSALAGVVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Similarity
| Similarity
                                                                                                                                                                                                                                                                                                                                      Yasunaga,
                                                                                                                                                                                                                                                                                                                                  Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii,
asunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                    ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <0LS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11;
Pred. No.
                                                                                        Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                         18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
0.0017;
                                                                                          DB 2;
. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151
                                                                                                            Length 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                              ×
:
                                                                                                                                                                                                                                                                                                                                             Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                              Yokoyama,
                                                                                                                                                                                                     GSPDB:GN00154
                                                                               0
                                                                                                                                                                                                                                                                                                            coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                              O157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and CsgB
a coli th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of c
                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                      RI
```

Вþ δÃ

C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 C;Accession: H85665 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Di

Plunkett III, G.; Burland, V.; Mau, B.; Glasner,

J.D.; Rose, Potamousis, 14-Sep-2001

Apoda

hypothetical protein

Escherichia

csgA [imported] -la coli

Escherichia

coli (strain 0157:H7, substrain

#text\_change

H85665 RESULT

```
A;Status: production A;Status: production A;A;Aclecule type: DNA
A;Residues: 1-439 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77578.1;
A;Cross-references: GB:BA000019; PIDN:BAB77578.1;
A;Cross-references: GB:BA000019; PIDN:BAB77578.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T36490
R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill submitted to the EMBL Data Library, July 1999
A;Reference number: Z21608
A;Accession: T36490
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                          DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An.

A:Peference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                      A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AF1813
                                                                                                                                                                                                                                                                                                                                                                                             AF1813
hypothetical protein alr0054 [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: bicyclomycin resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable transmembrane transport protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-152 <STO>
A;Residues: 1-152 <STO>
A;Cross-references: GB.AE005174; NID:g12514574; PIDN:AAG55788.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85665
                                                                                                                                                                                                        A; Reference number: AB1807; A; Accession: AF1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL;AL096822; PIDN:CAB46932.1; GSPDB:GN00070;
A;Exper1mental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene:
                                                                              A;Gene:
                                                                                                                                                                                                                                                                                                                                                                               C; Species: Anabaena sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-436 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
 Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                 'Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GSALAGVV 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                              alr0054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCOEDB: SCGD3.10c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        csgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSALAGVV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSALAGVVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSALAGVVPQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conserv
 Similarity
8; Conserv
 5.3%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
Library, July 1999
                     .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .08;
   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
 Score 8; DB 2
Pred. No. 5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
5, 5;
                 . 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                               PID:g17135032; GSPDB:GN00179
                                                                                                                                                                                                                                                                                     Ξ
:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #text_change 17-Mar-2000
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.
                                     Length 439
                                                                                                                                                                                                                                                                                   Sasamoto, :
M.; Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
 Indels
                                                                                                                                                                                                                                                                                   S.; W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPDB:GN00145; UWGP:Z1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                    Watanabe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCOEDB: SCGD3.10c
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                       :
                                                                                                                                                                                                                                                                                                      Α.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
 0
                                                                                                                                                                                                                                                                                     Tabata,
                                                                                                                                                                                                                                                                                                      Iriguch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             м
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
T34611
                 C;Accession: D89920
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                        conserved hypothetical protein SA1261 [imported] - Staphylococcus aureus (strain C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus
                                                                                                                                                                       D89920
                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T36447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

```
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, submitted to the EMBL Data Library, June 1999 A;Reference number: Z21549
                                                                                                                                                                     A; Experimental source: strain A3(2) C; Genetics:
                                                                                                                                                                                                                                                                                    R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, July 1999
A;Reference number: Z21598
A;Accession: T36447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2 C;Keywords: membrane-associated complex; NAD; oxidored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-552 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 [similarity] - Streptomyces C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-May-2000
                                                                                                                                                                                                          A;Cross-references: EMBL:AL096837; PIDN:CAB48911.1; GSPDB:GN00070;
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-62 <SEE>
                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T36447
                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SCF43A.24c - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: nuoN; SCOEDB: SC10A7.08c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AL078618; PIDN:CAB44518.1; GSPDB:GN00070; SCOEDB:SC10A7.08c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T34611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: T34611
                                                                           Matches
                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
39
                                     55 AALALQS
                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                     SCOEDB: SCF43A.24c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAAFAAIV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAAFAAIV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SALAGVVP
AALALQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALAGVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane-associated complex; NAD; oxidoreductase
                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                           Conservative
45
                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.3%;
                                                                                           4.6%;
                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                           Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8;
Pred. No.
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                               .
DB
                                                                                           .
.
.
.
.
                                                                           0
                                                                                                             Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.; Barrell, B.G.; Rajandream
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                B.G.;
                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                            SCOEDB: SCF43A.24c
                                                                                                                                                                                                                                                                                                                                              Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                           0
                                                                                                                                                                                                                                                                                                                                                м
.
А
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coel
```

; Cui, L.; Sekimizu,

..

```
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89920
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <KUR>
A;Cross-references: GB:BA000018; PID:913701226; PIDN:BAB42521.1; GSPDB:GN00149
                                                                                                                                                                                                                                                    C;Accession: AH2344
C;Accession: AH2344
R;Kaneko, T; Nakamura, Y; Wolk, C.P; Kuritz, T; Sasamoto, S; Watanabe, A; 11+9uv.
Nakazaki, N.; Shimpo, S; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superrum--;
F; 160-232/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Schuller, A.G.; Groffen, C.; van Neck, J.W.; Zwarthoff, E.C.; Drop, S.L. mol. Cell. Endocrinol. 104, 57-66, 1994
A;Title: cDNA cloning and mRNA expression of the six mouse insulin-like growth factor bi A;Reference number: 148600; MUID:95121750
A;Accession: 148605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C;Accession: I48605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain N315 C; Genetics:
                                                                                                                                                                                                   Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene:
                                                                                                                                                                                                                                                                                                                           ATP-binding protein of ABC transporter alr4311 [imported] - Anabaena sp. (strain C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin-like growth factor binding protein-6 - mouse
                                                                                                                  A; Cross-references: GB
A; Experimental source:
                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-251 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: IGFBP-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X81584; NID:g550386; PIDN:CAA57274.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-238 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: insulin-like growth factor binding protein 1; 160-232/Domain: thyroglobulin type I repeat homology <THY1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
              Matches
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; nes 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 ELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SA1261
                                                                                   alr4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSALAG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSALAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
              Conservative
                                                                                                                   GB:BA000019; I
ce: strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; 5u
100.0%; Pr
                              4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; pred No
                                                                                                                   PIDN:BAB76010.1; PID:g17133447; GSPDB:GN00179 2 7120
                0;
                              Score 7; I
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ore 7; DB 2; red. No. 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB .
                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 145;
                0;
                                                Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thyroglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:g550387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type I repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                  0;
                                                                                                                                                                                                                                                                                               Iriguch
                                                                                                                                                                                                                                                                                                                                                                                    PCC
                                                                                                                                                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-254 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вþ
probable zinc-finger protein [imported] - A
C;Species: Arabidopsis thaliana (mouse-ear
C;Date: 02-Feb-2001 #sequence_revision 02-F
C;Accession: A84682
                                                                                                                                                                                                                                                                             A;Gene: BMEII0506
A;Map position: II
C;Superfamily: oligopeptide permease protein oppB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI3572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                         Дb
                                                                        A84682
                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 LVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 VVSGSAL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VVSGSAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 7; Conserv
                                                                                                                                         84 AAFAAIV 90
                                                                                                                                                                                                                              Local
                                                                                                                                                                           7 AAFAAIV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LUNGTAS
                                                                                                                                                                                                          l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:AL513382; PIDN:CAD09543.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.6%;
                                                                                                                                                                                                                              4.6%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7; DB 2
Pred. No. 32;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                  0
                                                                                                                                                                                                                              Score 7;
Pred. No.
                                                                                                                                                                                                                  Mismatches
                   02-Feb-2001 #text_change 16-Feb-2001
                                                        Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB .
                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
```

```
, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A, Title: The genome sequence of the facultative intracellular pathogen Brucella melit. A; Reference number: AD3252; PMID:11756688
A, Accession: A13572
A, Statence, Section 113572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sa;Reference number: AB0502; PMID:11677608

A;Accession: AE0940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable ribulose-phosphate 3-epimerase STY3790 [imported] - Salmonella enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AE0940 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligopeptide transport system permease protein oppC [imported] - Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 C;Accession: AI3572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Ctth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-276 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53748.1; PID:g17984674; GSPDB:GN00191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PID:g16504659; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
0;
                                                     Length 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Church .; Farr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sdus
```

```
M.; Koul., X.; Koul. S.; Rouisley, S.D.; Shea, T. P.; Behito, M.I.; Town, C.D.; Puyli, C.Y.;
M.; Moo. H.; McTett, K.S.; Crolin, L.A.; Shan, M.; Yankker, S.E.; Umayam, L.; Tillon, L.
Nititler, Sequence And analysis of chromosome 2 of the plant Arabidopsis thaliana.
A: Accession Angles 20420; MUI:20063487
A: Status: Preliminary
A: Alexandres: CH:AR002093; NID:94803961; FIDN:AAD29833.1; GSPDB:6N00139
A: Cesse Lit. 202300
A: Sep Dosition: 2
C:Superfamily: Arabidopsis thaliana hypothetical protein F1284.290

Ourry Match
A: Solves thaliana hypothetical protein F1284.290

Oy 14 VSSSALA 20

Oy 14 VSSSALA 20
Search completed: O: Mismatches 0: Indels 0: Gaps 0;
Db 168 VSSALA 21

Search completed: Seconder 11, 2002, 21:20:42

Job time: 22 secs
```

### THIS PAGE BLANK (USPTO)

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                   Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              웆
                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                           Maximum
                                                                                                                                                                                                                                                                                                                                                                                                   Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                    Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein -
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                           BG
                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                          seq
 6666666666666677777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-543-407-5
151
1 MKLLKVAAFAAIVV
                                                                                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          October 11, 2002, 21:14:58; Search time 11 Seconds (without alignments) 531.514 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                          SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyright
 Length
GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                    먑
PTHP_LACCA
PTHP_LACLA
PTHP_LACSK
PTHP_LACSK
IMBA_RAT
AP4A_MOUSE
FLAV_DESDE
YZ30_METJA
YU95_MYCTU
CHED_BACTU
ATPE_ENTHR
ATPE_GALSU
                                                                                               FOLC_HUMAN
FOLC_MOUSE
RN12_MOUSE
RN12_MOUSE
PRH_ARATH
HMOH_AGRIP
AHM3_ARATH
PTHP_STRMU
PTHP_STRMU
PTHP_STRBO
PTHP_STRSL
YAF2_BACLI
VAL2_BACLI
                                                                                                                                                                                                                                         CSGA_SALTY
CSGA_ECOLI
RL20_PSEFL
RL20_PSESY
                                                                                                                                                                                         EFTU_CHACO
YHB0_YEAST
                                                                                                                                                                                                         IBP6_MOUSE
YTZ4_AGRVI
MHPB_ECOLI
EFTU_CYTLY
                                                                                                                                                                                                                                                                                   Ħ
                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                   105224
                                                                                                                                                                                                        P55225 salmonella
P28307 escherichia
O9x6e8 pseudomonas
P52828 pseudomonas
P47880 mus musculu
P70796 agrobacteri
P54711 escherichia
P42474 cytophaga l
        045932
045932
04447
0487485
075819
045896
094586
094586
094549
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
0958193
                                                                                                                                                                                                                                                                                 Description
                                                                                        8 saccharomyc
2 homo saplen
0 mus musculu
7 mus musculu
7 mus musculu
7 arabidopsis
9 agrotis ips
4 arabidopsis
6 streptococc
8 streptococc
6 streptococc
6 streptococc
6 streptococc
6 streptococc
6 streptococc
1 streptococc
8 streptococc
1 streptococc
9 sacillus 11
1 sbacillus 11
l bacillus su
l enterococcu
l galdieria s
                                                                                                                                                                                                cytophaga l
chara conni
              mycobacteri
bacillus su
                                 methanococc
                                        mus musculu
desulfovibr
                                                        lactobacill rattus norv
                                                                        lactococcus
lactococcus
```

45.	44	43	42	41	40	39	38	37	36	ဌဌ	34
σ	σ	σ	6	σ	σ	O	σ	0	σ	σ	σ
4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
248	247	244	240	236	235	235	226	226	211	210	203
1	$\vdash$	ᆫ	Н	Н	ᆫ	_	ب	Н	Н	Н	_
PCN2_SULOH	SNAB_MOUSE	CBR2_MOUSE	PYRH_AQUAE	UNG_CHLPN	YDJZ_ECOLI	RS4E_THEAC	GPH_VIBCH	BIOD_XYLFA	LEXA_XYLFA	UPP_DEIRA	CHPE_PSEAE
-		P08074 mus musculu		Q9z7d3 chlamydia p	P76221 escherichia		Q9knv6 vibrio chol		xylella	Q9ru32 deinococcus	O87005 pseudomonas

## ALIGNMENTS

RN [2]  RP SEQUENCE FROM N.A.  SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  RA MCDLINE=21534948; PubMed=11677609;  RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  RA Waterston R., Wilson R.K.;  RI Mature 413:852-856(2001).  RI Mature 413:852-856(2001).  RI SEQUENCE FROM N.A.  RA SPECIES=S.typhi; STRAIN-CT18;  RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  RA CLURCHER C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  RA Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  RA Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  RA Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  RA Whitehead S., Barrell B.G.;  RT "Complete genome sequence of a multiple drug resistant Salmonella enterita serovar Typhi CT18.";  RN MEDLINE=21646512; PubMed=8550497;  RN MEDLINE=21646512; PubMed=8550497;  Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;  RT Salmonella enteritidis agfHAC operon encoding thin, aggregative	OC Saltorella; Proteobacteria; gamma subdivision; Enterobacteriaceae; OC Salmonella.  OX NCBI_TaxID-602, 601, 592; RN [1]  RP SEQUENCE FROM N.A.  SPECIES=S.typhimurium; STRAIN-SR-11; RC SPECIES=S.typhimurium; STRAIN-SR-11; RX MEDLINE-98117058; PubMed-9457880; RX MEDLINE-98117058; PubMed-9457880; RX ROmling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; RR Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; RR "Curli fibers are highly conserved between Salmonella typhimurium and RT Escherichia coli with respect to operon structure and regulation."; RL J. Bacteriol. 180:722-731(1998).	GA_SALTY CSGA_SALTY CSGA_SALTY CSGA_SALTY CSGA_SALTY CSGA_SALTY CSGA_SALTY O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) Major curlin subunit precursor (Fimbrin SEF17 CSGA OR AGFA OR STM1144 OR STM1181. Salmonella typhi, and Salmonella typhi, and Salmonella enteritidis.  Racteria: Proteohacteria gamma subdivision:
--	--	--

```
RESULT 2
CSGA_ECOLI
                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                     δÃ
OC GREET DE AC
                                                                                                                                                  B
                                                                                                                                                                    δÃ
                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                       Query
Best I
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=91310586; PubMed=1677357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fimbriae.";
                                                                                                                                                                                                                                                                                                                                                      SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Purification and characterization of thin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collinson S.K., Emoedy L., Mueller K.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 21-33
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                               Major curlin s
CSGA OR B1042
                                                    01-OCT-1996
16-OCT-2001
                                                                         P28307;
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                           Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                    StyGene;
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
          Bacteria;
                      Escherichia
                                                                                                                                                  121
                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol.
                                                                                                                                                                                            61
                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLICOLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY ATTEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: STRONG, TO E.COLI CSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEMPERATURES FIBRONECTIN.
                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                              ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                        AJ002301; CAA05317.1; -. AE008749; AAL20074.1; -. AL627269; CAD08268.1; -.
                                                                                                                                                                                                                                                                               151;
                                          T-1996 (Rel. 34, Last sequence up
T-2001 (Rel. 40, Last annotation
curlin subunit precursor.
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                         Signal;
                                                                                                                                                                                                                                                                                                                                                                                     SG10608; csgA.
            proteobacteria;
                                                                                                                                                                                                                                                                                                                        151
                     coli
                                                                                                                                                                                                                                                                                                                                            21
134
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178:662-667(1996).
                                                                                                                                                                                                                                                                                                                                                                                               AAC43599.1; -.
                                                                                                                                                                                                                                                                                                                        ΑĀ;
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM
                                                                         24, Created)
                                                                                                                                                                                                                                                                                                                                             20
151
151
                                                                                                                                                                                                                                                                                                                        15305 MW;
                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A
            gamma
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                  MAJOR CURLIN SUBUNIT.
SVMVRQVGFGNNATANQY ->
REF. 5).
                                                                                                                                                                                                                                                                                         Score 151; DB 1;
Pred. No. 6.8e-144;
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                         B7DAC0D16B621359 CRC64;
                                                                                                                                                                                                                                                                               Mismatches
             subdivision;
                                                                update)
                                                                                                151
                                                     update)
                                                                                                ΑÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trust T.J., Kan, aggregative
              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                               '
                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                               DSYTQVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay w.w.;
/e fimbriae
                                                                                                                                                                                                                                                                                                      151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURLI AF
T GROWTH
                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARE
                                                                                                                                                                                                                                                                                 0;
```

```
SEQUENCE OF 21-40.
SERAIN=K12 / YMEL;
STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J., Ru
"The Crl protein activates cryptic ge
fibronectin binding in Escherichia co
Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for product
"Expression of two csg operons is required for product
"Expression of two csg operons is required for product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97061202; PubMed-8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K. Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The RpoS sigma factor relieves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=K12 / W3110;
                                         use by modified
                                                                                                                                                                                                                                                                                                                                                                                                                   Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repression of csgA, Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93211294; PubMed=8459772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                        MEDILINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T.J., "Purification and characterization of salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence Science 277:1453-1474(1997)
           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                          SIMILARITY: SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiol. 7:523-536(1993).
                                                                                                                                                        FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A
                                                                                                                                                                                                                                                                                      OF 21-31.
                                                                                                                             STRONG, TO SALMONELLA CSGA.
TO CURLIN MINOR SUBUNIT (CSGB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H-NS-mediated transcriptional
gene of fibronectin-binding c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  required for production curli polymers in Esche
                                                                                                                                                                                                                                                                                                                               Russell D.G., Normark S.; genes for curli formation coli HB101.";
                                                                                                                                                                                                                                              of thin,
                                                                                                                                                                                                                                                            Kay W.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rode C.K., Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                              coli K-12 genome
on the linkage map.";
                                                                                                                                                                                                                                              aggregative fimbriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.T., Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia
                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                       TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    curl1
                                                              is in
                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            വ
                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                         CURLI
                                                                                                                                                                                          GROWTH
                                                                                          outstation
                                                in no way commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLI
                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                            on
```

```
밁
                    ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQ ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                 Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D90742; BANGE CSGA.

ECOGene; EC11489; CSGA.

ECOGene; EC11489; CSGA.

Fimbria; Signal; Complete proteome.

SIGNAL 1 20
MAJOR C
7 A -> E
7 C003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RL20_PSEFL
Q9X6E8;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                   Blumer C., Heeb S., Pessi G., Haas D.;

"Global GacA-steered control of secondary metabolism in Pseudomonas fluorescens acts on specific ribosome binding sites.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS OF THAT SUBUNIT (BY SIMILARITY).

OF THAT SUBUNIT (BY SIMILARITY).
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                              PRINTS: PRO0062; RIBOSOMALL20.
PRODOM: PD002389; RIBOSOMALL20: 1.
PROSITE: PS00937; RIBOSOMALL20: 1.
RIBOSOMAL L20: 1.
                                                                                                                                                                             EMBL; AF136400; AAD34789.1; -. InterPro; IPR001081; Ribosomal_L20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CHAU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas fluorescens
104 AAFAAIV 110
                                                 Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SGSALAGVVPQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SGSALAGVVPQ 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L; L04979; AAA23616.1; -.
L; X90754; CAA62282.1; -.
L; AE000205; AAC74126.1; -.
L; D90741; BAA35832.1; -.
L; D90742; BAA35840.1; -.
          AAFAAIV 13
                                                                                                                                                                 PF00453; R1bosomal_L20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA;
                                                                                                    118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 39, Created)
(Rel. 39, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15049 MW;
                                             100.08; FI
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last
L20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                    ¥.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation
                                               Score 7; DB 1; Pred. No. 7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11; DB 1; L
Pred. No. 0.00095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAJOR CURLIN SUBUNIT.
A -> E (IN REF. 1).
; C003470D208D395F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                   E83E5775681EE452 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
                                                            DB 1;
5. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonadaceae;
                                                                         Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                 Gaps
                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
```

```
В
                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                             IBP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RL20_PSESY
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitten T., Willis D.K.;

"Suppression of a sensor kinase-dependent phenotype in Pseudomona syringae by ribosomal proteins L35 and L20.";

J. Bacteriol. 178:1548-1555(1996).

-i- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AN NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOM SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCT OF THAT SUBUNIT (BY SIMILLARITY).
                                                                                                                                 P47880;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update
Insulin-like growth factor binding protein (IBP-6) (IGP-binding protein 6).
IGFBP-6 OR IGFBP-6.
                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00062; RIBOSOMALL20.

PRODOM; PD002389; RibOSOMALL20; 1.

PROSITE; PS00937; RIBOSOMALL20; 1.

RibOSOMal protein; rRNA-binding.

SEQUENCE 118 AA; 13314 MW; 2BF171F5681EE443 CRC64;
MEDLINE-95121750; PubMed-7529732; Schuller A.G.P., Groffen C., van Drop S.L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RL20_PSESY
P52828;
                                        TISSUE=Liver;
                                                                                             Mammalia; Eutheria;
                                                                                                         Eukaryota; Metazoa;
                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001081; Ribosomal_L20
Pfam; PF00453; Ribosomal_L20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96198155; PubMed=8626280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SUPP27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas syringae (pv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996
                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U44118; AAB05016.1; -.
                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                 IBP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
                                                                                                                                                                                                                                                                                               104 AAFAAIV 110
                                                                                                                                                                                                                                                                                                                        7 AAFAAIV 13
                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (Rel. 34, Created)
6 (Rel. 34, Last sequ
1 (Rel. 40, Last anno
mal protein L20.
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                             Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                            4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    syringae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                            Score 7;
               van Neck J.W.,
                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7. 
; Mismatches
                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                           n update)
rotein 6 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                              238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                              DB 1;
5. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                              Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
             Zwarthoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                             precursor
                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                            Length 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bУ
                                                                                                                                                           (IGFBP-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SI
                                                                                                                                                                                                                                                                                                                                                 0
```

```
YTZ4_AC
ID YTZ4_AC
ID YT
AC P7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                    ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth fac
Mol. Cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use
                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seq
16-OCT-2001 (Rel. 40, Last ann
Hypothetical 31.6 kDa protein
Agrobacterium vitis (Rhizobium
                                                                                                                                                                                                                                                                     YTZ4_AGRVI
P70796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00121; IB;
SMART; SM00211; TY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000867; IGFBP.
InterPro; IPR000716; Thyroglobulin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                     MEDLINE=96252899;
                                                           SEQUENCE FROM N.
                                                                                             NCBI_TaxID=373;
                                                                                                               Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                               AGRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00222; IGF_BINDING; FALSE_NEG.
PROSITE; PS00484; THYROGLOBULIN_1; 1.
Growth factor binding; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:96441;
                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: O-GLYCOSYLATED.
SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                        SGSALAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pr00219; IGFBP; 1.
pr00086; thyroglobulin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                      SGSALAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cloning and mRNA expression of the six mouse insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P24593; 1BOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X81584; CAA57274.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
7; Conserv
                                                                                                                                                     pTrAB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%;
Jurity 100.0%;
Conservative
7 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tor binding proteins.
Endocrinol. 104:57-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
30
41
58
72
79
160
199
212
238
                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Igfbp6
                     PubMed=8672817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
45
64
85
105
188
210
232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                       7, Last sequence update)
0, Last annotation update)
Da protein in TAR-I TTUC'
(Rhizobium vitis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104:57-66(1994)
                                                                                                                                     alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THYROGLOBULIN TYPE BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
78
78
78
78
78
78
78
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INSULIN-LIKE GROWTH FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN 6
                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 7; DB 1
red. No. 14;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCEDC1D6AD9D59F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY.
                                                                                                                                       subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                                                                                                                           280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1
). 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                       Rhizobiaceae group
                                                                                                                                                                                             3'region (ORFZ4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
```

```
ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
               Federspiel N., Hyman R., Kalman S.
Namath A., Oefner P., Roberte P.
Submitted (NOV-1006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement or send an emeal?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHPB_ECOLI STANDARD; PRT; 314 AA. p54711; p77461; p77048; 01-CCT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 01-MAR-2002 (Rel. 41, Last annotation update) 2,3-dihydroxyphenylpropionate 1,2-dioxygenase MHPB OR B0348 OR Z0446 OR ECS0403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salomone J.-Y., Crouzet P., de Ruffray P., Otten L.; "Characterization and distribution of tartrate utilization genes the grapevine pathogen Agrobacterium vitis."; Mol. Plant Microbe Interact. 9:401-408(1996).
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=K12 / CS520; Ferrandez A., Garci
                                                                                                                                                                                                                                                                                                               Spence E.L., Kawamukai M., Sanvoisin J., Braven H., "Catechol dioxygenases from Escherichia coli (MhpB) eutrophus (MpcI): sequence analysis and biochemical third family of extradiol dioxygenases."; J. Bacteriol. 178:5249-5256(1996).
                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / W3110;
MEDLINE=96359381; PubMed=8752345;
Spence E.L., Kawamukai M., Sanvoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32375; AAB61632.1;
                                                                                                                                         Gregor J., Davis N.W., Kirkpatrick H.A., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                 "The
                                                                                                                                                          Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                    Science
                                                                                                                                                                                             STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SGSALAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSALAG 188
                                                                                                                  complete genome sequence nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; Figure an AA; 31571 MW;
                                                                                                                                                                                                                                                                Garcia
                                                                                                                                                                                                                                                                                                                                                                                                                                    83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.6%;
                                                                                                                                                                                                                                                 ţo
                                                                                                                                                                                                                                                                J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid.
                                        Roberts D.,
                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma subdivision;
                                                                                                                                                                                                                                                                Diaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                 of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89050A6A81A55A61 CRC64;
                                      Aparicio A.M., Chung E., S., Komp C., Kurdi O., Le ., Schramm S., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no resing as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                 coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EC
                                                  Chung E.
                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.13.11.-).
                                                                                                                                                                                                                                                                                                                                         , Bugg T.D.H.;
) and Alcaligenes
l properties of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                  Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        outstation
                                                        Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    commerci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĺ'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on
                                                        D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
```

SEQUENCE

```
RESULT 8
EFTU_CYTLY
ID EFTU_CYTLY
AC P42474;
                                                                                        멍
                                                                                                                 Ş
                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                  Matches
                                                                                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.", Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                           Pfam; PF02900; LigB; 1.
Oxidoreductase; Dioxygenase;
Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D86239; BAA13053.1; -. EMBL; Y09555; CAA70748.1; -. EMBL; AE000142; AAC73451.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyam Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli" O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Overproduction, purification and properties of 2,3-dihydroxyphenylpropionate 1,2-dioxygenase from Escherichia coli." Biochim. Blophys. Acta 1202:258-264(1993).
-!- FUNCTION: EXTRADIOL CLEAVAGE OF 2,3-DIHYDROXYPHENYLPROPIONIC -!- COFACTOR: FURROXY FURROXYPHENYLPROPIONATE DEGRADATION PATHWAY.
-!- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                            EcoGene; EG20274; mhpB.
                                                                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-15, MEDLINE=94002258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-0157:H7 / F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / EDL933 / ATCC 700927; MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                        276 VAAFAAI
                                                                                                                    6 VAAFAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: TO A.EUTROPHUS MCPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                       U73857; AAB18072
                                                                                                                                               Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              IPR004183;
                                                                                                                                                                                                           314
                                                                                                                                                                                                                         172
138
152
157
                                                                                                                                                Conservative
                                                                                                                    12
                                                                                                                                                                                                           8
               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CHARACTERIZATION PubMed=8399388;
                                                                                                                                                                                                                         171
314
140
152
157
                                                                                                                                                                                                           34196 MW;
                                                                                                                                                              4.6%;
                                                                                                                                                                                                                                                                                                                                            LigB.
                                                                                                                                                              Score 7; pred. No
                                                                                                                                                                                                          ING -> NKA (IN REF.
R -> H (IN REF. 1).
A -> T (IN REF. 1).
W; ElD5A8574E5DFE05
                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                Aromatic
                 PRT;
                                                                                                                                                Mismatches
                                                                                                                                                              No.
                 395
                                                                                                                                                                                                                                                                                                                hydrocarbons catabolism;
                                                                                                                                                                            DB 1;
                                                                                                                                                              18;
                                                                                                                                               0,
                                                                                                                                                                            Length 314;
                                                                                                                                                                                                          CRC64;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K., Yokoyama
M., Tobe T.,
                                                                                                                                               0
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>~</u>
```

```
OX OOR DET DACE
                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                          Query Match
Best Local S
Matches 7
                                                                  EFTU_CHACO
P50371;
01-OCT-1996
01-OCT-1996
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995
01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                         NP_BIND
SEQUENCE
                                                                                                                               _CHACO
                                                                                                                                                                                                                                                                                  Elongation factor; Protein biosynthesis; GTP-binding.
NP_BIND 19 26 GTP (BY SIMILARITY).
NP_BIND 81 85 GTP (BY SIMILARITY).
NP_BIND 136 139 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU, 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antonie Van Leeuwenhoek 64:285-305(1993).

-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94368062; PubMed=8085791;
Ludwig W., Neumaler J., Klugbauer N., Brockmann E., Roller C.
Klugbauer S., Reetz K., Schachtner I., Ludvigsen A.,
Bachleitner M., Fischer U., Schleifer K.H.;
"Phylogenetic relationships of Bacteria based on comparative
Chloroplast.
Eukaryota; Viridiplantae;
NCBI_TaxID=13779;
                                 Chara connivens.
                                                          Elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytophaga lytica
Bacteria; CFB gro
NCBI_TaxID=979;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X77035; CAA54324.1; -. HSSP; P02990; 1EFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis of elongation factor Tu and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elongation
                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                              170
                                                                                                                                           9
                                                                                                                                                                                                     13 VVSGSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                             VVSGSAL
                                                                                                                                                                                                                            Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                               PR00315; ELONGATNFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.
                                                                                                                                                                                                                                                                                                                                   PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     990; 1EFU.
IPR000795;
                                                          6 (Rel.
6 (Rel.
8 (Rel.
factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 (Rel.
5 (Rel.
1 (Rel.
factor
                                                                                                                                                                                                                                                                         136
395 A
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group;
                                                                                                                                                                                                                                                                         ΑA;
                                                                                                                    STANDARD;
                                                        34, Last sequence up 37, Last annotation Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32,
40,
Tu
                                                                                                                                                                                                                                                                         42973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2. Created)
2. Last sequence up
3. Last annotation (EF-Tu).
                                                                                                                                                                                                                         4.6%; Score 7; DB
100.0%; Pred. No. 22
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flavobacteria;
                                                                                           Created)
           Streptophyta; Characeae;
                                                                                                                                                                                                                                                                        MW; 6FA7C1CF90C72C89
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-synthase
                                                                                                                    408
                                                                                                                                                                                                                               DB .
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions
                                                                                                                    B
                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELONGATION FACTOR
                                                                                                                                                                                                                                                 ·Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellulophaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.
                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAMILY
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                          0
```

```
SO THE TEXT OF THE PROPERTY OF
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPRO00795; GTP_EFTU.
InterPro: IPRO04161; GTP_EFTU_D2.
InterPro: IPRO04160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D2: 1.
Pfam; PF03144; GTP_EFTU_D2: 1.
Pfam; PF03144; GTP_EFTU_D3: 1.
Pfam; PF03143; GTP_EFTU_D3: 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=95392822; PubMed=7663757;
MEDLINE=95392822; PubMed=7663757;
Delwiche C.F., Kuhsel M., Palmer J.D.;
Phylogenetic analysis of tufA sequences indicates
"Phylogenetic analysis of tufA sequences indicates
origin of all plastids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995
01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHB0_YEAST
P38748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use
                                    Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirst Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E. J., Maori C., Mardis E., Menezes S. Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vyignati D., Wilcox L., Wohldman P., Waterston R., Wilson F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02990; 1EFU.
Mendel; 13588; CHACO; TufA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                               STRAIN=S288C / AB972;
MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                      Hypothetical YHL010C.
                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota;
Saccharomycetales; Saccharomyc
              Vaudin M.;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 VVSGSAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phylogenet. Evol. 4:110-128(1995).
FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EMEuropean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS.
SUBCELLULAR LOCATION: (
SIMILARITY: BELONGS TO
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVSGSAL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U09425; AAA87685.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             non-profit institutions as long a and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
81
136
408
                                                                                                                                                                                                                                                                                                                                                                                               5 (Rel. 31, Created)
5 (Rel. 31, Last sequ
1 (Rel. 40, Last anno
al 67.5 kDa protein i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor; Protein biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
85
139
                                                                                                                                                                                                                                                                                                         Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45321 MW;
                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
protein in PRPS4-STE20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast.
O THE GTP-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; DAA452E42B0C3489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                  Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
). 23;
                                                                                                                                                                                                                                                                                                            Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage by
                                                                                                                                                                                                                                                                                                                                                                                                      intergenic region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 408;
                                                                                                                                                                                                                                                                                                                                  Saccharomycetes;
                                                                                                                                           C., Kirsten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyanobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                            s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL
                                                                         Vaughan
                                                                                                                                             Dover
sten J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration -
MBL outstation -
                                                                                                 Mouser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ċ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                      J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

```
RESULT 11
FOLC_HUMAN
IDC_HUMAN
IDC_HUMAN
IDC_Q059;
DT 01-00
DT 01-00
DT 01-00
DT 01-00
DT FPGS
GN FPGS
RM GDLL
RN [2]
RD FISS
RX MEDLL
RN FISS
RX MEDLL
RN [3]
RP FISE
RN FISE
RX MEDLL
RN FISE
RY FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGD: S0001002; YHL010C.

SGD: S0001002; YHL010C.

InterPro: IPR001841; Znf_ring.

InterPro: IPR001607; Zf-UBP.

Pfam; PP00097; Zf-G3HC4; 1.

Pfam; PF02148; Zf-UBP; 1.

SMART; SM00184; RING; 1.

SMART; SM00290; ZnF_UBP; 1.

PROSITE; PS00518; ZF_RING_1; FAL

PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced the Swiss Institute of Bioinformatics Institute. There are the European Bioinformatics Institute. There are the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide VIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 265:2077-2082(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; ZN_FING 240 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U11582; CAB34905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Folylpolyglutamate synthase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOLC_HUMAN Q05932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                          chen
Freemantle S.J., Taylor S.M., Krystal G., Moran R.G. "Upstream organization of and multiple transcripts folylpoly-gamma-glutamate synthetase gene.";
J. Biol. Chem. 270:9579-9584(1995).
                                                                                                                                                                                                                                                         Garrow T.A., Admon A., Shane B.;
"Expression cloning of a human cDNA encoding
                                                                                                                                                                                                                                                                                                                                  TISSUE=Lymphocytes;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 20-587
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Folylpoly-gamma-glutamate synthetase) (FPGS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452
                                                                                          MEDLINE=95238480; PubMed=7721888;
                                                                                                                                                                                                               folylpoly(gamma-glutamate) synthetase and determination
primary structure.";
                                                                                                                                                                                                                                                                                                       MEDLINE=93028422; PubMed=1409616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 QTASDSS 134
                                                                                                                                        SEQUENCE
                                                                                                                                                                                       Proc.
                                                                                                                     rISSUE-Placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO C.ELEGANS EEEDB: 9 AND S.POMBE SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S46825; S46825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTASDSS 458
                                                                                                                                                                                         Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               OF 1-353 FROM N.A.
Qi H., Korenberg J.
d (JUL-1995) to the
                                                                                                                                           OF 1-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                             FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280
                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67503 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinc-tinger
                                                                                                                                                                                                                                                                                                                                                                                                                     MN.A.
                                                                                                                                             N.A.
                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Shane
                                                                                                                                                                                              89:9151-9155(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88FF670CC73A1263 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It is produced through a collaboration informatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                    В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.POMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 585
                                                                                R.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPAC16E8.13
                                                          from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC
                                                          the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

```
RESULT 12
FOLC_MOUSE
ID FOLC_MOUSE
                                                                                                                                                                                         멍
                                                                                                  S
                                                                                                                                            Query Match
Best Local
                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M98045; AAA35852.1; A
EMBL; U14939; AAA87568.1; -
EMBL; U40868; AAA87568.1; J
EMBL; U40863; AAA87568.1; J
EMBL; U40865; AAA87568.1; J
EMBL; U40865; AAA87568.1; J
EMBL; U40866; AAA87568.1; J
EMBL; U40867; AAA87568.1; J
EMBL; U40867; AAA87568.1; J
EMBL; U40867; AAA87568.1; J
EMBL; U40867; AAAC13871.1; J
EMBL; U44253; AAC13871.1; J
PTR; A46281; A46281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clchowicz D.J., Shane B., Clchowicz D.J., Shane B., Mammalian folylpoly-gamma-glutamate synthetase. 1. Purification "Mammalian folylpoly-gamma-glutamate synthetase."; general properties of the hog liver enzyme."; Blochemistry 26:504-512(1987).

-i- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.
ALLOWS TISSUES TO CONCENTRATE FOLATE AT HIGHER LEVELS THAN IN
                                                                                                                                                                                                  INIT_MET
NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                          HSSP; P15925
MIM; 136510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taylor S.M., Freemantle S.J., Moran R.G.;
"Structural organization of the human folypoly-gamma-glutamate synthetase gene: evidence for a single genomic locus.";
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; 1.

PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; 1.

Ligase; One-carbon metabolism; ATP-binding; Mitochondrion;
                                                                                                                                                                                                                                                                                                                               InterPro; IPR001645; FOLYLPOLYGLU_SYNT InterPro; IPR004101; Mur_ligase_C. Pf0m; PF02875; Mur_ligase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87157665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetase gene: evidence for a Cancer Res. 55:6030-6034(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96105015; PubMed=8521387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 102-587 FROM
                                                                         305
                                                                                                  54 NAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORD
BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FF
SIMILARITY: BELONGS TO THE FOLYLPOLYGLUTAMARE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + [tetrahydrofoly1-[Glu]](N) + L-glutamate = ADP + phosphate + [tetrahydrofoly1-[Glu]](N+1). SUBUNIT: MONOMER.
                                                                         NAALALQ 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M98045; AAA35852.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                               15925; 1FGS.
6510; -.
                                                                                                                               Similarity
7; Conserv
                                                                                                                                                                                                                                                                         peptide; Alternative
                                                                                                                                                                                  43
103
22
587
                                                                                                                               Conservative
                                                                                                    60
                                                                                                                                                                                      ₹
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=3828320;
                                                                                                                                                                                                    42
587
43
109
22
                                                                                                                                                                                        64609 MW;
                                                                                                                                           4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED
                                                                                                                               0:
                                                                                                                                                                                                                      HITTALIA MITOCHONDRION.
FOLYLPOLYGLUTAMATE SYNTHASE
TO OVTOPLASMIC ISOFORM.
                                                                                                                                                                                                    FOR CYTOPLASMIC ATP (POTENTIAL). I -> V (IN REF.
                                                                                                                                                                                                                                                                            initiation
                                                                                                                                            Score 7;
Pred. No.
    PRT;
                                                                                                                                                                                      5AF81409F5F77E5C
                                                                                                                               Mismatches
                                                                                                                                                                                                                 (POTENTIAL).
  587
                                                                                                                                            DB 1;
). 32;
                                                                                                                             0
                                                                                                                                                        Length 587;
                                                                                                                                                                                      CRC64;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
                                                                                                                             0
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          о
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          way
                                                                                                                             0
```

```
Best
 Matches
                         Query Match
                                                                 CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                              INIT_MET
                                                                                                                                                                         TRANSIT
CHAIN
                                                                                                                                                                                                                             InterPro; irver_ligase; 1.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF01225; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Different antifolate-resistant L1210 cell variants with either increased or decreased folylpolyglutamate synthetase gene expression at the level of mRNA transcription.";
J. Biol. Chem. 270:26918-26922(1995).
                                                                                                                                                                                                           PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; 1. PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; 1. Ligase; One-carbon metabolism; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: ATP + {tetrahydrofoly1-[Glu]}(N) + L-glutar = ADP + phosphate + {tetrahydrofoly1-[Glu]}(N+1).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL GENE PRODUCES BOTH FORM:
-!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORM:
BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRA-
-!- SIMILARITY: BELONGS TO THE FOLYLPOLYGLUTAMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spinella M.J., Brigle K.E., Goldman I.D.;
"Molecular cloning of murine folylpoly-gamma-glutamate synthetase.";
Biochim. Biophys. Acta 1305:11-14(1996).
-i- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES. TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P48760:
01-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY 2000 (Rel. 39, Last annotation update)
Folylpolyglutamate synthase, mitochondrial pro
                                                                                                                                                                                                                                                                                                        EMBL; U33557; AAC52812.1;
EMBL; U32197; AAC52426.1;
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
                                                     SEQUENCE
                                                                                                                                                                                                                                                                   MGD; MGI:95576; Fpgs.
InterPro; IPR001645; FOLYLPOLYGLU_SYNT
                                                                                                                                                                                                                                                                                                                                                  or send
                                                                                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DBA/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                HSSP; P15925; 1FGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96180977; PubMed=8605241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96070787; PubMed=7592937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Folylpoly-gamma-glutamate synthetase) (FPGS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLOWS TISSUES TO CONCENTRATE FOLATE AT HIGHER LEVELS
Similarity
7; Conserv
                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                  1
43
43
103
103
27
27
35
75
129
129
138
491
491
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Mouse)
                                                                                                                                                                                                    Alternative
                                                                                                                                                                        587
                                                                   109
27
35
76
129
138
                                                     64907
              4.6%;
100.0%;
                                                     WW;
                                                             FOLYLPOLYGLUTAMATE SYNTHATE
FOR CYTOPLASMIC ISOFORM.
ATP (POTENTIAL).
P -> A (IN REF. 2).
G -> W (IN REF. 2).
QL -> HV (IN REF. 2).
R -> S (IN REF. 2).
D -> E (IN REF. 2).
G -> S (IN REF. 2).
 0;
              Score 7; Pred. No
                                                                                                                                                                                                    initiation
                                                                                                                                                                                       MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                     B43FB8915EB64E05
Mismatches
              NO.
                         DB
              32;
                          <u>ب</u>
                                                                                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                             Usage
0;
                         Length 587;
                                                     CRC64;
                                                                                                                                                                        SYNTHASE
Indels
                                                                                                                                                                                                                                                                                                                                                                            Ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC
                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          + L-glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.3.2.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THAN
                                                                                                                                                                                                                                                                                                                                                                                           is in
                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
0
                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
Gaps
                                                                                                                                                                                                                                                                                                                                                                             commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAME.
                                                                                                                                                                                                                                                                                                                                                                                           5
0
```

Qγ

54 NAALALQ

= = =

Вb

305

NAALALO

```
RESULT 14
PRH_ARATH
                                                                                                                                                                                                                  DI AC
                                                                                                      밁
                                                                                                                               δõ
                                                                                                                                                           Matches
                                                                                                                                                                        Query Match
Best Local :
    PRH_ARATH
P48785;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bach I., Rodriguez-Esteban C., Carriere C., Bnushar Rose D.W., Glass C.K., Andersen B., Izpisua Belmont Rosenfeld M.G.;
"RLIM inhibits functional activity of LIM homeodoms factors via recruitment of the histone deacetylase Nat. Genet. 22:394-399(1999).

-i- FUNCTION. ACTS AS A NEGATIVE CO-REGULATOR FOR TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RN12_MOUSE
Q9WTV7;
                                                                                                                                                                                                                               DOMAIN
ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                               SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                       Transcription
                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1342291;
                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Opposing developmental functions of positive and negat coregulators of LIM homeodomain factors."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99364422; PubMed=10431247;
Bach I., Rodriguez-Esteban C., Carriere C.,
Rose D.W., Glass C.K., Andersen B., Izpisua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNF12
                                                                                                      443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RING finger LIM domain-binding protein) (R-LIM)
                                                                                                                                34 GGGNSSG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEACETYLASE COREPRESSOR COMPLEX.
                                                                                                     GGGNSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CT-2001 (Rel. 40, Created)
CT-2001 (Rel. 40, Last sequence update)
CT-2001 (Rel. 40, Last annotation update)
CT-2001 (Rel. 40, Last annotation update)
finger protein 12 (LIM domain interacting RING
                                                                                                                                                                                                                                                                                                                       MGI:1342291; Rnf12.
Pro; IPR001841; Znf_ring.
PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                                                                                 AF069992; AAD34209.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR RLIM
                                                                                                                                                                                                                                                                                                                                                                                         s requires a license agreement (Some mail to license@isb-sib.ch).
                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                               600 AA;
                                                                                                                                                                                                                                         on regulation;
415 484
546 587
     (Rel. 33, Created)
                                                                                                                                                           Conservative
                                                                                                     449
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                461
66470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
                                                                                                                                                                       100.0%;
                                                                                                                                                                                     4.68;
                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                      Zinc-finger.
SER-RICH.
                                                                                                                                                         Score 7; DB 1; Pred. No. 32; 0; Mismatches
                                                                                                                                                          0;
                                                                                                                                                                                                                             POLY-SER
                                                                                                                                                                                                                                          RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                             E68299530126E41D CRC64;
                                  796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600
                                                                                                                                                                    DB 1;
). 32;
                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homeodomain transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bhushan A.,
Belmonte J.
                                                                                                                                                                                  Length 600;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      finger protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMEODOMAIN
SIN3A/HISTONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krones
                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α.
                                                                                                                                                         Gaps
                                                                                                                                                       0;
```

```
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Ram Modijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Ram Modijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Ram Modijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Ram Modijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Ram Modijman P., Klein Lankhorst R., De Clercq R., Ram Modigman M., Wallarroel R., De Clercq R., Ram Modigman M., Rogers J., Cronin A., Quali M., Bray-Allen S., Ray M., Lennard N., McLay K., Mayes R., Ram Modigman M., Loehaert M., Grimm M., Loehaert T.-H., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehaert T.-H., Ram Borkova D., Bloecker H., Scharfe M., Grimm M., Loehaert D., Herzl A., Ram Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Ram Ramsenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Ram Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Ram Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Ram Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Ram Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Francs P., Bielke C., Ram Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Ram Schonking T., Kallcki J., Graves T., Harmon G., Edwards J., Ram E., Johnson S., Scholler P., Cordes M., Abu-Threideh J., Ram E., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Ram Aller P., Bentley L., Cloud J., Abbott A., Scott K., Johnson D., Ram Aller P., Bentley S., Scholler P., Schafes M., Abu-Threideh J., Ram E., Johnson J., Pietch J., Bergheff A., Jones K., Drone K., Cotton M., Joshu C., Ram Aller P., Zhong J., Preston R., Will D., Shekher M., Pepin K., Hillier L., Ram D., Johnson J., Pietch J., Bergheff A., Jones K., Drone K., Cotton M., Joshu C., Ram Aller M., Berghawa A., Hameed A., Lodhi M., Johnson A., Ram C., Shohdy N., Hasegawa A., Hother M., Matter A., Shah R., Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mayer K.F.X., Schweller C., Wambutt R., Murphy G., Volckaert G., Pooli T., Duesterhoeft A., Stlekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Brandt P., Bother G., Ramsperger U., Hilbert H., Braum M., Meltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braum M., Indien R. Paradt P., Deters S., Wan Garveren M., Nitzes W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. COLUMBIA; MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA;
MEDLINE=98012533; PubMed=9351248;
Plesch G., Stoermann K., Tovar Torres J., Walden R., Somssich I.E.;
"Developmental and auxin-induced expression of the Arabidopsis prhahomeobox gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Pathogenesis-related homeodomain protein (PRHA).
PRH OR PRHA OR AT4G29940 OR FZ7B13.180.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rorfhage U., Trezzini G.F., Meier I.,
"Plant homeodomain protein involved in
a pathogen defense-related gene.";
Plant Cell 6:695-708(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. COLUMBIA;
MEDLINE=94312876; PubMed=7913642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12:635-647(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hahlbrock K., Somssich I.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcriptional regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosidae;
```

```
RRRRR OCCOOC
                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                      ş
                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR001965; PHD.
Pfam; PF00046; homeobox; 1.
Pfam; PF00628; PHD; 1.
SMART; SM00389; HOX; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                   HMDH_AGRIP
076819;
16-0CT-2001
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
DUPORTHELS L., ROSSIGNOL F., Couillaud F.;
PMOLECULAR cloning and tissue expression of 3-hydroxy-3-methylglutaryl
"Molecular cloning and tissue expression of 3-hydroxy-3-methylglutaryl
"Molecular cloning and tissue expression of 3-hydroxy-3-methylglutaryl
coenzyme A reductase of the black cutworm Agrotis ipsilon.";
"""""
""" | The definition of the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                Agrotis ipsilon (Black cutworm moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Plerygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Noctuinae; Agrotis.
                                                                                                                                                          reductase).
                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-hydroxy-3-methylglutaryl-coenzyme A reductase
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL050352; CAB43669.1; -. EMBL; AL161575; CAB79752.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana.";
Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                   309
                                                                                                                                                                                                                                                                                                         ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           send
                                                                                                                                                                                                                                                                                   NGGGNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: SPECIFICALLY BINDS TO THE FUNGAL DNA ELEMENT, 5'-CTAATTGTTTA-3', OF THE GENE SUBCELLULAR LOCATION: NUClear. INDUCTION: BY PATHOGEN INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                        NGGGNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L21991; AAA32843.1; -. U48864; AAC49836.1; -.
                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding; Nuclear protein; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                    452
6052
632
713
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                        39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROT entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         НОМЕОВОХ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                252
303
511
735
631
658
685
712
735
                                                                                                                                                                                                                                                                                                                                                                           759
90657
                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                     4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEN INFECTION.
TO THE PHD-AS
                                                                                                                                                                                                                                                                                                                                                                          MΨ;
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                    Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                HOMEOBOX.
5 x 27 AA
1.
                                                                                                                                                                                                                                                                                                                                                                                    5 (INCOMPLETE)
LEUCINE-ZIPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHD-TYPE.
ASP-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHD-ASSOCIATED FAMILY
                                                                                                                                                                                                                                                                                                                                                                         5E61509A0CAD6175 CRC64;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA TANDEM REPEATS
                                                                                                                                                                                                                            833
                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions in as its content is in
                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                  Length 796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELICITOR-RESPONSIVE PR2 PROMOTER.
                                                                                                                                                                  (EC
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ьy
                                                                                                                                                                  1.1.1.34) (HMG-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            윾
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outstation
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             по
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            way
                                                                                                                                                                                                                                                                                                                            0
```

Search completed: October 11, 2002, 21:19:28 Job time: 12 secs

```
밁
                                       QY
                                                                                                                                                                      $\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\text{$\
                                                                                 Matches
                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use European Bioinformatics Institute of Bioinformat use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement.
                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                   TRANSMEM
ACT_SITE
ACT_SITE
ACT_SITE
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoprene biosynthesis;
DOMAIN 1 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0071; HMGCOARDTASE.
PROSITE; PS00066; HMG_COA_REDUCTASE_1;
PROSITE; PS0031B: HMG_COA_REDUCTASE_3;
PROSITE; PS01192; HMG_COA_REDUCTASE_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00368; HMG-CoA_red; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002202;
InterPro; IPR000731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ009675; CAA08775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
  682
                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEROL ISOPRENOIDS, WHICH ARE ESSENTIAL FOR GROWTH DIFFERINTIATION (BY SIMILARITY).

CATALYTIC ACTIVITY: (R)-mevalonate + CoA + 2 NADP(+) hydroxy-3-methylglutaryl-CoA + 2 NADPH.

ENZYME REGULATION: THE ACTIVITY OF HMG-COA-REDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: SYNTHESIS OF MEVALONATE FOR THE PRODUCTION STEROL ISOPRENOIDS, WHICH ARE ESSENTIAL FOR GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUPPRESSED BY EXOGENOUS MEVALONATE. PATHWAY: ISOPRENOID BIOSYNTHESIS.
                                          SGSALAG
SGSALAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PS50065; 
; PS50156;
                                                                                                     Similarity
                                                                                 Conservative
                                                                                                                                                                                                                                                     322
420
10
91
160
301
504
711
809
680
715
688
                                       21
                                                                                                                                                                      ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMG_COA_REDUCTASE_4;
SSD; 1.
                                                                                                                                                                                          32
117
180
321
504
711
809
680
715
720
813
                                                                                                                                                                                                                                                                                                                                                                                                                                             419
833
                                                                                                                                                                      89789
                                                                                                   4.6%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HMG-CoA_red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADP
                                                                                                                                                                   MW;
                                                                                                                                                        POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OCHORAL BASE (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                 0;
                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEMBRANE - BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic reticulum; Transmembrane;
                                                                                 Mismatches
                                                                                        e 7;
No.
                                                                                        DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ng as its content is in
                                                                                                                       1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                 0;
                                                                                                                       Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADP(+)
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    γģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဝှ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  = (S)-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON-
                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      commerciai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          way
                                                                               0
```

#### THIS PAGE BLANK (USPTO)

```
Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
::
                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB DB
                                                                                                                                                                                                                                                     d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-543-407-5
151
1 MKLLKVAAFAAIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October 11, 2002, 21:15:28 ; Search time 27 Seconds (without alignments) 967.490 Million cell updates/sec
                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562222 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 60.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                          sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                  sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                        sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                             sp_mammal: *
                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_fung1:*
                                                                                                                                                                                                                                                                                                                                                                   sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                   sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                          sp_virus:*
                                                                                                                                                                                               Length
  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapext 60.0
                                               10
16
2
                                  16
                                                                             033802
054069
0984T8
0983J5
093U24
093U24
09XA68
09XA68
09XA91
09XA91
          0 09SDX8
0 099U60
09AE10
09CLF5
09AQD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chosen
                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parameters:
                               033802 salmonella
054069 salmonella
09r4t8 salmonella
09r3j5 escherichia
09x3j5 escherichia
09xa68 streptomyce
09xa77 streptomyce
09xa77 streptomyce
09xa91 streptomyce
0911c0 streptomyce
0911c0 streptomyce
099160 staphylococ
09ae10 corynebacte
09colf pasteurella
          Q9aqd9 lactococcus
Q91x24 mus musculu
                                                                                                                                                                                              Description
Q94an7 arabidopsis
```

45	44	43	42	41	40	39	38		36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
					٠											٠					٠			٠	•		4.6	
413	404	404	396	396	395	395	391	388	387	378	367	358	351	347	325	323	320	320	317	317	315	311	305	304	303	284	284	268
2	N	2	6	σ	4	4	11	S	16	5	16	10	œ	10	თ	10	2	ν	16	10	N	10	11	w	w	10	10	10
Q51691	Q9K4Y8	Q9K4Z3	Q95JW6	Q95JX2	Q96KC9	Q96M17	Q9D4L4	044529	005313	076736	Q92A84	Q9FG34	Q9BAB4	Q9C6X9	Q9XU26	Q9MA45	Q9K418	Q9КНС9	Q981S2	023220	Q9L1T5	Q9LNY7	Q9CR05	Q92194	Q96W96	Q9SL35	Q42375	Q9FIQ2
Q51691 paracoccus	moritella	moritella	Q95jw6 macaca fasc	macac	homo	homo	4	Ω	005313 mycobacteri	lictyostel	Q92a84 listeria in	Q9fg34 arabidopsis	Q9bab4 polytoma ob	9	o.	Q9ma45 arabidopsis	Q9k418 streptomyce	s		023220 arabidopsis	Q911t5 streptomyce	Q9lny7 arabidopsis	(J)		a)	s135	375	Q9fiq2 arabidopsis

## ALIGNMENTS

```
δã
                              В
                                                       δÃ
                                                                                        Ъ
                                                                                                                     δÃ
                                                                                                                                                                                                               033802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
                                                                                                                                                   Query Match
Best Local Similarity
Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O33802 PRELIMINARY;
O33802;
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98053981; PubMed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes interaction of
                                                                                                                                                                                                            Infect. Immun. 65:5320-5325(1997).

EMBL; AJ000514; CAA04151.1; -.

NON_TER 152 152

SEQUENCE 152 AA; 15401 MW; 9DA
                                                                                                                                                                                                                                                                        Salmonella typhimurium SR-11 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=602;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGFA PROTEIN (FRAGMENT).
 140 VGFGNNA 146
                                                          90
                                                                                          20
                                                                                                     20 AGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGA 79
                                              DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQ 139
                                                                                        AGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGA 79
                              DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQ 139
                                                                                                                                              84.1%; Score 127; DB 2; Lot 100.0%; Pred. No. 5.5e-117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                               15401 MW; 9DA7DADC2364B006 CRC64;
                                                                                                                                                                                                                                                                                       aggregative fimbriae promotes interaction of um SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                Length 152;
                                                                                                                                                 Indels
                                                                                                                                                   0
                                                                                                                                                   Gaps
                                                                                                                                                   0
```

밁

140

VGFGNNA 146

```
밁
                 Š
                                                                                                                                                                                                                                                              RESULT
Q9R4T8
                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Thes 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q54069
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                 Query Match
Best Local
                                                                                                                                                                                                             Q9R4T8
Q9R4T8;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2000
                                                                    Stolpe H., Grund S., Schrouer w., "purification and partial characterization of type salmonella typhimurium var. copenhagen."; Int. J. Med. Microbiol. Virol. Parasitol. Infect. E SEQUENCE 19 AA; 1910 MW; 9AD8B59D411E5B51 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q54069;
Q54069;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cox J.M., Eglezos S., Woolcock J.B.;
"Virulence of Salmonella enteritidis in chickens correlates colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                              MEDLINE~95102231; PubMed=7803933;
                                                                                                                                           SEQUENCE
                                                                                                                                                             NCBI_TaxID=602;
                                                                                                                                                                        Salmonella.
                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                         Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U53207; AAA98671.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SE30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEF17 FIMBRIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLIEGL 01, 01-NOV-1996 (TREMBLIEGL 01, 01-DEC-2001 (TREMBLIEGL 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=592;
                   21 GVVPQWGGGGNHN 33
                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                 34
 Н
                                                                                                                                                                                                                                                                                                                                              S
GVVPQWGGGGNHN 13
                                                                                                                                                                                                                                                                                                                                          3 FIMBRIAE (FRAGMENT).
                                                                                                                                                                                                                                                                                                      QNGFRNNATIDQ
                                                                                                                                                                                                                                                                                                                        QNGFRNNATIDQ
                                         13;
                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           76 AA;
                                                                                                                                                                                                           (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
                                       Conservative
                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     76
                                                                                                                                                                                                                                                                                                                          105
                                                                                                                                                                                                                                                                                                                                                                                                                          7704 MW;
                                                                                                                                                                                                                                                                                                                                                                              47.7%; 500
100.0%; Pr
                                                8.6%;
100.0%;
                                                                                                                                                                                gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                       0;
                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB; pred. No. 4e-
0; Mismatches
                                                Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          2FD5411241A7BCB1
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                      Mismatches
                                                                                                                                                                              subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subdivision; Enterobacteriaceae;
                                                 No.
                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
4e-63;
                                                           DB 2;
                                               1.4e-05;
                                                                                                                                                                                                                                                     ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÃΑ
                                                                              Infect. Di
B51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 76;
                                                                                      Dis.
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                          3 fimbriae from
                                                                                       281:8-15(1994)
                                      0;
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                               93
                                      0;
                                                                                                                                                                                                                                                                                                                                                                                   0
```

RESULT

₽ 4 (

```
RESULT
Q9XA68
ID QS
AC QS
DT 01
DT 01
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSS3J5
AC Q99
AC C90
AC
                                                                                                                                                                                                                                          QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q93U24
                                                                                                                                                                                                   Вb
                                                                                                                                                                                                                                                                                                                                                                          Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
    Q9XA68;
Q9XA68;
01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-43895 RED VARIANT;

MEDLINE-21218556; PubMed=11319125;

Whlich G.A., Keen J.E., Elder R.O.;

"Mutations in the csgD Promoter Associated with Variations Expression in Certain Strains of Escherichia coli 0157:H7."

Expression in Certain 67:2387-2370(2001).

EMBL; AF275733; AAK53212.1; -.

EMBL; AF275733; AAK53212.1; -.

EMBLGE 152 AA; 15099 MW; EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q93U24;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9S3J5;
Q9S3J5;
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coll.
Escherichia coll.
Racteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSGA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q93U24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coll 078:K80 iso
"S1 inserti on in CsgB and reduced persistence
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -.
NON_TER 29 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAR-2001 (TYEMBLrel. 16, Last annotation update)
CURLIN SUBUNIT MONOMER (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSPOSON=INSERTION SEQUENCE IS1; MEDLINE=99314153; PubMed=10386375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                    σ
                                                                                                                                                                                                   15
                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 SGSALAGVVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                               5 SGSALAGVVPQ
|||||||||||
5 SGSALAGVVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSALAGVVPQ
                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                         Similarity
    (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 AA; 2789 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli
                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                                       .7.3%;
    12,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision;
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,;
                                                                                                                                                                                                                                                                                                         Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E290DFC07ABBB243 CRC64;
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                          436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; 0.0018;
                                                                                                                                                                                                                                                                                                       DB 2;
0.0077
                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolates associated with ce in poultry infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                           Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 29
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOUR RESERVED TO COLUMN TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XAR7
Q9XAR7;
Q1-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                        STRAIN=A3(2);
Bentley S.D.,
Submitted (JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUTATIVE T
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; aset of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY EMBL; AL096822; CAB46932.1; -- Interpro; IPR003662; sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                 STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane.
SEQUENCE 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            James K.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saunders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Redenbach M., Kieser H.M.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           set of ordered cosmids and a detailed genetic and e 8 Mb Streptomyces coelicolor A3(2) chromosome."; 1. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSALAGVV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSALAGVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V-1999 (TrEMBLrel. 1
C-2001 (TrEMBLrel. 1
NADH DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o
                                                                                                                                                                                                                                                                                                        D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE TRANSPORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (2);
                                                                                                                                                                                                                                                                                (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JUL:1999)
                                                                                                                                                                        .D., Parkhill J., I
(JUN-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
DEHYDROGENASE SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.3%; Sillarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill J., Barrell B.G., Rajandream M.A.;
JUL:-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      coelicolor.
                                                                                                                                                                                                                                                                                                        Harris
                                                                                                                                                                                                                                                                                                                                                                                                        Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45991
                                                                                                                                                                                                                                                                           ţ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 0
                                                                                                                                                                                                                                                                                                                                                                                                    Actinobacteria; Actinobacteriaa ptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
                                                                                                                                                                        Barrell B.G., Rajandream M.A.;
e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Denapaite D.,
                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFD05F0FD59FCA49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e 8;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552
                                                                                                                                                                                                                                                                                                                                                                                                                              Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eichner A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٧,
                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                     physical map
                                                                 Cullum
                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cullum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
Q9XA91
  QΥ
                                                                                                                                                                   Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SO DR
                                                                 Q9L1C0
                                                                          RESULT 9
                                                                                                  Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЪ
                                                                                                                                 Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                  Q9XA91;
01-NOV-1999 (TrEMBLrel. 12, Cre
01-NOV-1999 (TrEMBLrel. 12, Las
01-DEC-2001 (TrEMBLrel. 19, Las
HYPOTHETICAL 6.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      James K.D.
Submitted
                       Q9L1C0;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).

EMBL; AL096837; CAB48911.1; -
Streptomyces
         PUTATIVE INTEGRAL MEMBRANE SCL11.18.
                                                                                                                                                                Hypothetical protein SEQUENCE 62 AA; 6
                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
                                                          Q9L1C0
                                                                                                                                                                                                                                 MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                          STRAIN=A3(2)
                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                         Seeger K., Harris D., Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                  Seeger K.,
                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                  SCF43A.24C..
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9XA91
                                                                                                                                                                                                                         Redenbach M., Kieser H.M.,
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                 55
                                                                                                  39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                 AALALQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAAFAAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAAFAAIV
                                                                                                  AALALQS
                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conser
                                                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                 ., Parkhill
(JUL-1999)
                                                          PRELIMINARY;
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                  45
                                                                                                                 61
 coelicolor
                                                                                                                                                                                                                                                                                                                                 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                        Streptomycineae;
                                                                                                                                                                  6605 MW;
                                                                                                                                         4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.3%;
100.0%;
                                                                                                                                                                                                                                                                 J.,
                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                        Actinobacteria; Actinobacterida ptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                 Barrell B.G., Rajandream M.A.;
the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                        Denapaite D.,
                 PROTEIN
                         Last
Last
                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                         Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8;
Pred. N
                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                          Score
Pred.
                                                                                                                                                                 7F6AF8437BE11B00
                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A74E40FEA914ED77 CRC64;
                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                        sequence up
annotation
                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
                                                                                                                                     e 7;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO.
                                                          138
                                                                                                                                                                                                                                                                                                                                                    Actinobacteridae;
Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB .
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                 DΒ
                                                                                                                                         30;
                                                          Ą
                                                                                                                                                                                                                         Eichner
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
                        update)
on update)
                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAD(+) +
                                                                                                                                 0;
                                                                                                                                                Length 62;
                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 552
                                                                                                                                                                                                                         Α.,
                                                                                                                                                                                                  and
e.";
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                         Cullum
                                                                                                                                                                                                        physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UBIQUINOL
                                                                                                                                                                                                                         ٠
;
                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                         for
                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

4

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
  Matches
                                                                       "Phosphoenolpy.uvu---
regulated at the level of expression.,
Plant J. 20:33-342(1999).

Plant J. 20:33-342(1999).

-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AP203403; AAF19404.1; -.

InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0007290; Ser_thr_pkinase.
Pfam; PP00069; pkinase; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                   Q9SDX8 PRELIMINARY; PRT; 145 AA.
Q9SDX8;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE (FRAGMENT).
                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerdeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                        Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Brassi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 8 Mb Streptomyces coelicolor A3(2) Mol. Microbiol. 21:77-96(1996). EMBL; AL157953; CAB76405.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20040078; PubMed=10571893;
MEDITURE=2, Gill A., Nimmo G.A., Wilkins M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach M.,
                                                                   NON_TER
                                                                                                                                                                                                                      Nimmo H.G.;
                                                                                                                                                                                                                                                                            NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 SALAGVV 23
|||||||
54 SALAGVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                  10
         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          set of ordered cosmids and a detailed genetic and physical map
Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.M., Parkhill J., Fed (FEB-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FEB-2000)
                                             1
145
145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AA;
 4.6%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kieser H.M., Denapaite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.;
                                                         1
145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08; **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14825 MW;
                                               16023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrell B.G., Rajandream M.A.;
e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7;
  Score 7; DB 1
Pred. No. 64;
0; Mismatches
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36D3391E13A919EA CRC64;
                                               A90350EA032457F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB .
              DB 10;
o. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome.
                                                                                                                                                                                                                                                                                           Brassica.
                                                                                                                                                                                                                                                                                                             Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eichner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                     core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 138;
   0;
                       Length 145;
                                                                                                                                                                                                                                  Jenkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cullum
                                                                                                                                                                                                                                                                                                                 Tracheophyta;
                                                                                                                                                                                                                                  G.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٦.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
   0;
                                                                                                                                                                                                                                                                                                      Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
    0;
```

δÃ

. Q

42 DSTLSIY

```
A TO CONTROL OF THE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q99U60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
RESULT
Q9AE10
ID QS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC13032;
MEDLINE=99361031; PubMed=9695918;
Mehmeier L., Schafer A., Burkovski J.;
Malke H., Puhler A., Kalinowski J.;
"The role of the Corynebacterium glumetabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AE1;
Q9AE1;
Q9AE1;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence up
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation
HOLLIDAY JUNCTION DNA-HELICASE RUVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain Mu50). Bacteria, Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Staphylococcus QCBI_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrembLrel. 17, 01-JUN-2001 (TrembLrel. 17, 01-DEC-2001 (TrembLrel. 19, HYPOTHETICAL PROTEIN SA1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).
EMBL; AP003133; BAB42521.1;
EMBL; AP003362; BAB57590.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole genome aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SA1261 OR SAV1428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         099060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99U60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; SEQUENCE 145 AA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                  Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AE10
                                                                                               Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 ELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 ELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSTLSIY 52
  s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
Kalinowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                               144:1853-1862(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete
  ч.
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group; Staphylococcus
                                                                                                                                                                                               Burkovski A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
  Puhler
                                                                                                                                                                                                                                                                                                                                                                                                                        (Brevibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
(HYPOTHETICAL PROTEIN S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 1; Pred. No. 64; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome.
245ECA4104A63875 CRC64;
                                                                                                                                                glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1
                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacteridae;
                                                                                                                                                                                                 Kramer R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                             flavum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 145
                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAV1428).
                                                                                                                                                                                                       Mechold U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
```

```
RESULT OF THE PROPERTY OF THE 
RESULT

Q9AQD9

ID Q9

AC Q9

AC Q9

AC TO

DT 01

DT 01

DT 01

DT 01

DE LL

GN RH

OC LB

OC LB

OC LB

OC LB

OC ST

RP SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genomic sequence of Pasteurella M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006167; AAK03364.1; -.

Interpro; IPR000056; Ribul_P_3_epim.

Pfam: PF00834; Ribul_P_3_epim; 1.

Complete proteome.

SEQUENCE 229 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                             Q9AQD9;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9CLF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The role of Corynebacterium glutamicum secretion genes secD, secG in transporting the Streptomyces griseus alpha-amylase."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF038651; AAK19839.1; ...

EMBL; P40832; IBVS.

InterPro; IPR00383; HHH_1.

InterPro; IPR003085; RuvA.

Pfam; PF01330; RuvA; 1.
                                                                                                         RRB.
Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PF01330; RuvA; 1. Pfam: PF02904; RuvA_II; 1. ProDom: PD006268; RuvA; 1.
                                                                                                                                                                                                                                                                         Q9AQD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOD_1 OR PM1280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00278; HhH1; 1.
                                                                 Lactococcus
                                                                                      Bacteria; Firmicutes;
                                                                                                                                                          LLRRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 KVAAFAA 136
                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 13 VVSGSAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KVAAFAA 11
                                                                                                                                                                                                                                                                                                                                                                                  VVSGSAL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17,
L (TrEMBLrel. 17,
L (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 AA;
                                                                                                                                                                             (TrembLrel. 17, Created)
(TrembLrel. 17, Last seq
(TrembLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21476 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.6%;
                                                                                    Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; [
                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; 1
Pred. No.
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F8F0C96358C34E8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                         236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
5.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

SEQUENCE FROM N.A

```
Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                  RESULT
Q91X24
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
""thes 7; Conserve
                                                                                                                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                뫄
                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                             밁
time
                                                                                                                                                                                                                                                                                                           Q91X24
Q91X24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-20244638; PubMed-10784052;
O'Connell-Motherway M., van Sinderen D., Morel-Deville F.,
Fitzgerald G.F., Ehrlich S.D., Morel P.;
"Six putative two-component regulatory systems isolated from Lactococcus lactis subsp. cremoris MG1363.";
                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN
                                                                                                                                     SEQUENCE
                                                                                                                                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC012723; AAH12723.1; -.
                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00448; REC; 1.
DNA-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001789; Response
Interpro; IPR001867; Trans_re
Pfam; PF00072; response_reg;
Pfam; PF00486; trans_reg_C; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL TRANSDUCTION.
EMBL; AF176556; AAG53726.1;
HSSP; P08402; 1800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis subsp. cremoris MG1363.";
Microbiology 146:935-947(2000).
-i- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-MG1363;
                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                  TISSUE-COLON;
                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                           127 NQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                              124 NQTASDS 130
                                                                                                                                                                                                                                                                                                                                              15
completed: October 11,
ne : 29 secs
                                                                  15
                                             23
                                           SGSALAG
                                                                  SGSALAG
                                                                                                                                     238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AA;
                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                           29
                                                                 21
                                                                                                                                                                                                                              Rodentia;
                                                                                                                                                                                                                                       Chordata;
                                                                                                                                     25346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Response_reg_C.
                                                                                                  4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.68;
          2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                         0
                                                                                                   Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7;
Pred. No.
                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3DD5808FA45D0C4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sensory transduction;
                                                                                                                                     DDBAFD5DB0413CF7 CRC64;
          21:20:09
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                         Mismatches
                                                                                                   NO.
                                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                                                                                                                                                                                                DB , 97;
                                                                                                  DB 1
                                                                                                                                                                                                                                                                                                                       A
                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                           0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 236;
                                                                                                             Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                         Indels
                                                                                                                                                                                                                              Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                       0
```

# THIS PAGE BLANK (USPYO)

š

```
A. Geneseq_032802:*

1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
3: /SIDS1/gcgdata/
4: /SIDS1/gcgdata/
4: /SIDS1/gcgdata/
5: /SIDS1/gcgdat
5: /SIDS1/gcgdat
7: /SIDS1/gcgdat
8: /SIDS1/gcgdat
9: /SIDS1/gcgdat
10: /SIDS1/gcgd
11: /SIDS1/gcgd
11: /SIDS1/gcgd
11: /SIDS1/gcgd
13: /SIDS1/g
14: /SIDS1/g
15: /SIDS1/g
15: /SIDS1/g
16: /SIDS1/g
17: /SIDS1/g
18: /SIDS1/g
19: /SIDS1/g
20: /g
21: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                   Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on:
                                                                                                                                                                                                                                                                                                                                 and is
                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB DB
                                                                                                                                                                                                                                   Score
     773
768
693
692
691
689
683
                                                                                                                                                                                                                                                                                                                                                   greater than
                                                                                                                                                                                                                                                                                                                             No. is the number of results predicted by chance to have greater than or equal to the score of the result being puderived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-543-407-5
773
1 MKLLKVAAFAAIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     October 11, 2002, 21:03:23 ; Search time 32 Seconds (without alignments) 524.129 Million cell updates/sec
     100
100
89
89
89
89
89
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                     //SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                                                                                                                                                                                                                                   Length
     151
151
151
151
151
151
151
151
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3 (c) 1993 - 2002 Compu
                                                                                                                                                                                                                                     ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapext 0.5
       Ħ
     AAR74625
AAW33341
AAW336346
AAB36347
AAB36353
AAB36350
AAB36350
AAB36350
                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen Ltd
AgfA sequence. Sa Salmonella enterit Salmonella enterit AgfA::PT3#1 amino AgfA::PT3#2 amino AgfA::PT3#8 amino AgfA::PT3#8 amino AgfA::PT3#5 amino AgfA::PT3#5 amino AgfA::PT3#5 amino AgfA::PT3#5 amino AgfA::PT3#6 amino
                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                 printed,
```

thali	AAG29728	21	447	12.1	ω	٠.
Drosophila melanog	ABB66343	22	287		93.5	_
M. catarrhalis str	AAW68203	19	892		94	~
Salmonella enterit	AAB36336	21	19	12.4	96	
Salmonella enterit	AAB36328	21	19		96	
onel	AAB36323	21	19	•	96	_
æ	AAW56163	19	738	•	97.5	_
H. pylori bacteria	AAY78364	21	718	•	98	w
melanc	ABB62708	22	1028	12.7	98.5	~
Drosophila melanog	ABB65764	22	850	•	98.5	٠.
e encod	AAU08231	22	597	•	105	01
enteri	AAB36340	21	23	•	109	
enteri	AAB36324	21	23	14.1	109	~
Salmonella enterit	AAB36319	21	23	•	109	٠
a enteri	AAB36337	21	22	14.4	111	
Salmonella enterit	AAB36327	21	22	14.4	111	_
Salmonella enterit	AAB36322	21	22	14.4	111	•
	AAB36342	21	151	•	111.5	w
hia coli	AAB36344	21	151	14.6	112.5	_
Salmonella enterit	AAB36339	21	22		115	٠.
a enteri	AAB36325	21	22	٠	115	٠.
	AAB36320	21	22		115	-
enteri	AAB36338	21	23		123	~
	AAB36326	21	23	15.9	123	٠٠
enteri	AAB36321	21	23	•	123	_
enteri	AAB36318	21	22	17.1	132	_
nonella en	AAB36316	21	45	30.7	237	•
n. Esch	AAR52663	15	122	•	436	~
bind	AAR52664	15	142	65.7	508	_
a coli	AAB36343	21	151	•	586	٠.
ella enteri	AAW23569	18	120	•	588	٠.
equenc	AAR62761	15	120	76.1	588	_
::PT3#3 a	363	21	151	85.1	658	~
AgfA::PT3#10 amino	AAB36355	21	151	88.1	681	٠٠

# ALIGNMENTS

RESULT 1 AAR74625

```
Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                   WPI; 199
N-PSDB;
                                                                                                                                                                                                                                  AAR74625 standard;
                                                        Clouthier SC,
                                                                                                                                         WO9425598-A.
                                                                                                                                                         Salmonella.
                                                                                                                                                                      Salmonella; AgfA; vaccine
                                                                                                                                                                                     AgfA sequence
                                                                                                                                                                                                     26-JUN-1995
                                                                                                                                                                                                                    AAR74625;
                                                                    (KING/) KING J.
(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                             26-APR-1993;
                                                                                                             26-APR-1994;
                                                                                                                            10-NOV-1994.
                                   1994-358275/44.
DB; AAQ87467.
                                                                                                                                                                                                    (first entry)
                                                         Collinson
                                                                                             9305-0054452
                                                                                                             94WO-IB00207
                                                                                                                                                                                                                                  Protein;
                                                         SK,
                                                                                                                                                                                                                                  151
                                                         Doran
                                                                                                                                                                                                                                  AA
                                                         Кау
                                                         Æ
```

```
RESULT 2
AAB36341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SXCCCXX
    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant agfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologus species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       animals) and humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic immunization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig7B; 95pp; English
                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                              05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36341 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing
                                                                                                                                                                    Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                        2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151;
                                                                                                                                                                                                                                                                                                                     ΑP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA;
                                                                                                                                                                                                                                                                                                                     Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                              99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                       Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 773; DB 15; Pred. No. 1.8e-65;
                                                                                                                                                                                                                                                                                                                       SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                       Kay
                                                                                                                                                                                                                                                                                                                       WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                    animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

```
RESULT 3
AAW23570
ID AAW2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agria protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agra protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW23570 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                               Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis 27655-3b agfA.
          enteropathogenic bacteria of the
                        Isolated Salmonella gene agfA - used for diagnosis of Salmonella
                                                     WPI; 1997-309886/28.
N-PSDB; AAT74142.
                                                                                                                                                      26-APR-1994;
26-APR-1993;
                                                                                                                                                                                               26-APR-1993;
                                                                                                                                                                                                                         03-JUN-1997
                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                         (UYVI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKYAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                           VICTORIA INNOVATION & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                Collinson
                                                                                                                                                      94US-0233788
93US-0054452
                                                                                                                                                                                               93US-0054452
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 773; DB 21;
Pred. No. 1.8e-65;
Mismatches 0;
                                                                                                Doran
              Enterobacteria
                                                                                                                             CORP
                                                                                                Kay WW
                family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                or,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
```

Example 2; Fig

7;

85pp; English

```
CCCxpxpqqqxnxqxpxpxpxpxxxxxxxxxxxxdxxdXd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뭐
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from
The present invention describes a recombinant agfA gene segment of the gene has been replaced by a segment of a
                                               Disclosure;
                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                     WPI; 2000-672631/65.
N-PSDB; AAC64622.
                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                                                                       05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                  WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#1 amino acid sequence SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36346 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virtually all other microbial organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNPALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150;
                                                                                                                                                                                                Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AA;
                                           Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                           99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.48;
                                                                                                                                                                                                Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 768; DB 18;
Pred. No. 5.3e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                         response in animal
(I) where a foreign DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         It can also used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens. which may be important for directing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/RAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CsgA and AgfA-homologue fimbrin subunits, respectively: (2) directing recombinantion of a recombination of the homologous species; (3) directing recombination of a recombination of a recombination of the homologous species; (3) directing recombination of a recombination of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising generating and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                           Escherichia Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                    White AP,
                                                                                                                                    05-APR-2000; 2000WO-CA00356.
                                                                                                                                                                                                                       W0200060102-A2
                                                                                                                                                                                                                                                                                                     Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                             vaccine;
                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#2 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36347 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                          (UYVI-) UNIV VICTORIA.
                                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                           immune response;
                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 AA;
                                                                                                                                                                                                                                                                                  coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                  9905-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.9%;
90.1%;
                  Collison SK,
                                                                                                                                                                                                                                                                                                                                           immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 695; DB 21;
Pred. No. 4.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                      NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
```

2000-672631/65

```
cc segment of the gene has been replaced by a segment of a foreign DNA cc sequence which encodes a foreign epitope or antigen. Also described are: (c) use of thin aggregative fimbriae (SEFI/TAF) nucleation depended cc assembly system of strains of Salmonella, Escherichia coli and coll and cc interobacteriaceae for the production of fimbriae comprising recombinant agrae (SEFI) and (S
ARBSULT 6
AAB363
IID AAB3
IID AAB3
XX AAB6
AC AAB3
XX AAB6
XX AAB6
XX 26-F
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                 Synthetic
                                                                                                                                                                                                                                                                                AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36353 standard;
                                                                          Escherichia coli
                                                                                                                                                                                                                 Salmonella;
                                                                                                        Salmonella enteritidis
                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITOSGYGNGADVGOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pal Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC64623
                                                                                                                                                                                   immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                    agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                   response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.7%;
90.7%;
                                                                                                                                                                                      ımmunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 693; DB 21;
Pred. No. 6.5e-58;
3; Mismatches 11;
                                                                                                                                                                                                                    gene replacement; fimbrin; epitope:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

RESULT 7 AAB36349 ID AAB3

AAB36349 standard; Protein; 151 AA

AAB36349;

g

121

NNAALVNQTASDSSVMVRQVGFGNNATANQY

Gaps

0

120 120 60 60

```
В
                                                                                                                δÃ
                                                                                                                                                            Вb
                                                                                                                                                                                                    QУ
                                 ğ
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of the production of fimbriae comprising recombinant Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbriae subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinantion of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                   useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-672631/65.
N-PSDB; AAC64629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                 Sequence
                              121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                             61
                                                                                                                       61
                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                       MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQ
                                                                          LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                   SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                    151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-CA00356
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0127888
                                                                                                                                                                                                                                                                        89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison
                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                        Score 692; DB 21;
Pred. No. 8.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SK,
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay WW;
151
                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                           0
```

(I) is

26-FEB-2001

```
õ
                                                          밁
                                                                                       Ş
                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                     amino acid sequence or sequences grown on Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                     61
                                                          Н
                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                      ΑP,
                                                                                                                                                 Similarity
                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                       ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888
                                                                                                                                                 89.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen
                                                                                                                                                 Score 691; DB 2
Pred. No. 1e-57;
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW
                                                                                                                                                                   21;
                                                                                                                                                                   Length 151;
                                                                                                                                0
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are:
                                                                                                                                0;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                    AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                               sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively: (2) directing recombination of a recombination of the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant comprising separating an amino acid polymer comprising a recombinant
                                  immunogens, which may be important for directing an immune respagainst the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgfA::PT3#7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36352 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC64628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                    exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collison SK, Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogen
                  present invention
                                    given in
```

```
RESULT 9
AAB36350
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36350 standard; Protein; 151
comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the
                                                                   assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; replacing the native
                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA
                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                           Disclosure; Page 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                       copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                          2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEMAHANOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                             AAC64626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sequence SEQ ID NO:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.3%;
                                                                                                                                                                                                                            139pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 690; DB 21;
Pred. No. 1.2e-57
                                                                                                                                                                                                                                                                                                                                                                       SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                       Kay
                                                                                                                                                                                                                                                                                                                                                                       WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                           animal
                                                                                                                                                                            are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
```

```
RESULT 10
AAB36354
AAB36354
AC AAB36
XX AAB36
AC AAB36
AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                           WPI; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36354 standard; Protein; 151
                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                       2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137;
                                                                                                                                                                                                                                                                                                                                                                           ΑP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                 AAC64630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid sequence SEQ ID NO:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                           Page 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.1%;
90.7%;
                                                                                                        139pp; English
                                                                                                                                                                                                                                                                                                                                                                                 Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 689; DB 21;
Pred. No. 1.6e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
```

The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D segmence which encodes a foreign epitope or antigen. Also describe

DNA

are:

```
RESULT 11
AAB36351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising separating an amino acid polymer comprising a recombinant (Agra protein containing a replacement segment or segments of foreign amino acid seguence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the coplymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agra protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the protein to the carrier for the present sequence is given in the process of the carrier for the present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Agfa, Csga and Agfa-homologue fimbrian subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; not the homologous species.
WPI; 2000-672631/65
                                                          White AP,
                                                                                                                                                                                            05-APR-1999;
                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                            WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#6 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36351 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001 (first entry)
                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                            99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.4%;
90.1%;
                                                          Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 683; DB 21;
Pred. No. 5.7e-57;
1; Mismatches 14
                                                             Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

ş 밁 ş В Š

```
amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the protein the purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                  directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively: (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC64627
                                                   exemplification of the present invention.
```

Best Local Similarity Matches 137; Conserv 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 61 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120 ۳ 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG Conservative 88.2%; 90.7%; 2; Score 682; DB 21; Pred. No. 7.1e-57; Mismatches Indels 0 Gaps 120

Q DЬ Š

Query Match

Length 151;

0

Sequence

151 AA;

DЬ δ В

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

```
RESULT 12
AAB36355
PN XXX
                                      Salmonella enteritidis
                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                         26-FEB-2001
                                                                                                                                               AAB36355 standard; Protein; 151
                            Escherichia coli.
                                                                                     AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                         immune
                                                                                                        (first entry)
                                                       response;
                                                         immunogen
```

. .

WO200060102-A2

```
Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дβ
                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                               Qy
                                                                    AAB36348
XXXX
                                                    ij
                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
     _ AAB36348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfa gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Agfa, CsgA and AgfA-homologue fimbria subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2000
                                                    AAB36348 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA
                                                                                                                                              121
                                                                                                                                                                                    121
                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 137; Conserv
                                                                                                                                                                                                                                                                                               ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.
                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQV 151
                                                                                                                                                NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0127888
                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                           88.1%;
90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collison SK,
                                                      151
                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                           Score 681; DB 21;
Pred. No. 8.9e-57;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                      Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay WW.
                                                                                                                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                0
```

Qy

Дď

61 61

SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDQWNAKNSDITVGQYGG

```
뫄
                                 QΥ
                                                                                                                                                                                              back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrian protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and chexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                              Query Match
Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC64624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#3 amino acid sequence SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 136; 139pp; English.
                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                 Similarity
                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agfA; chromosomal gene replacement; fimbrin; epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888
                                                                                                                                                              AA;
                                                                                                 85.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                              Score 658; DB 21;
Pred. No. 1.3e-54;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay
                                                                                  12;
                                                                                                                      Length 151;
                                                                                  0;
                                                                                  Gaps
      60
```

~

Ş

밁

AAR62761 standard; Protein; 120 AA

```
ARESULT 14
AAR62761
ID AAR62
XX AAR62
XX AAR62
XX AAR62
XX AAR62
XX Salmc
XX Salmc
XX Salmc
XX Salmc
XX Salmc
XX IO-NC
X
                                                                                                                                                                                                                          RESULT 15
AAW23569
XXXXXXXX
                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                             á
                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-358275/44.
N-PSDB; AAQ73066.
                       Salmonella enteritidis 27655-3b TnphoA mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the Salmonella enteritis 27655-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clouthler SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritis 27655-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; AgfA; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR62761;
                                                                                  29-SEP-1997
                                                                                                                                                                                             AAW23569 standard; Protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig7A; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KING/) KING J.
(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9425598-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 76.1%; So
Local Similarity 100.0%; I
hes 112; Conservative 0;
                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VVPQWCGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                     GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                                                                                                                                                                                          GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AA;
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-IB00207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 588; DB
); Pred. No. 4.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.1e-48;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Кау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MM
                          agfA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 120;
                                                                                                                                                                                                                                                                                                                                        112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
```

```
Search completed: October 11, Job time : 33 secs
                                                                                      ОĀ
                                                                                                                   В
                                                                                                                                              Qy
                                                           Вb
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated Salmonella gene agfA - u enteropathogenic bacteria of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT74141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1994;
26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                     from virtually all other microbial organisms.
                                                           61
                                                                        82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                  1997-309886/28.
                                                         GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                                                                                          120 AA;
                                                                                                                                                                            76.1%; So ilarity 100.0%; If Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0233788
93US-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9308-0054452
               2002, 21:13:17
                                                                                                                                                                                          Score 588; DB 18;
Pred. No. 4.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for diagnosis of Salmonella
Enterobacteria family
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW;
                                                                                                                                                                                                         Length 120;
                                                                                                                                                                               Indels
                                                                                                                                                                               0.
                                                                                                                                                                             Gaps
                                                                                                                     60
                                                                                                                                                 81
```

#### THIS PAGE BLANK (USPTO)

```
Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
      22222211154
2222221176
22322221176
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                        Score
      588
97.5
94
92
92
92
89.5
89.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /ggn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 October 11, 2002, 21:12:43; Search time 17 Seconds (without alignments) 216.957 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-543-407-5
773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231628 seqs, 24425594 residues
     11.5
110.5
110.5
110.4
110.4
110.2
110.2
110.2
110.2
110.2
110.1
110.1
110.1
110.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALA........DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                        Length DB
     US-08-233-788A-59
US-08-233-788A-57
US-08-233-788A-57
US-08-233-788A-57
US-09-196-387-8
US-09-196-387-2
US-09-196-387-2
US-09-336-447A-13
US-09-336-447A-13
US-09-336-447A-13
US-09-336-447A-13
US-09-336-447A-13
US-08-808-599A-24
US-08-808-599A-24
US-08-804-227C-3
US-08-043-123-2
US-09-043-123-2
US-08-043-123-2
US-09-025-7698-280
US-08-458-298-280
US-08-541-780-2
US-08-541-780-2
US-08-541-780-2
US-08-687-379-4
US-08-172-332-1
US-08-687-379-4
US-08-968-685A-10
US-08-308-682-2
                                                                                                                                                                                                                                                                                                                                                                        IJ
                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231628
Sequence 59, Appli
Sequence 37, Appli
Sequence 3, Appli
Sequence 10, Appli
Sequence 110, Appli
Sequence 204, Appli
Sequence 204, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                        Description
```

Š

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

<b>M</b> B Q C	RESU US-C	
Query Matc Best Local Matches ]	SSULT 1 :08-23-788A- :08-23-788A- :08-23-788A- :08-23-788A- Sequence 59, Patent No. 56 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF I TITLE OF I TITLE OF I OUNTRY: CITY: S STATE: COUNTRY: STATE: COMPUTER R MEDIUM T COMPUTER R REFREENC TILING D CLASSIFI ATTORNEY/A REFREENC TELEFAN: TELEFAN: TELEFAN: TELEFAN: TYPE: ATOPOLOGY MOLECULE T TOBERECULE T TOBERECULT T TOBERECULT T TOBERECULT T TOBERECULT T TOBERECULT T T T T T T T T T T T T T T T T T T	4444433355 4444443365777777777777777777777777777777
	T 1 23-788A-59 uence 59, Application of the control	๑๑๑๑๓๓๓ 
h Similarity 50; Conserva	71 Call Trans Trans See Entropy 12 Call Trans See Entropy 12 Call Trans STEE Entropy 12 Call Trans STE	
99.4% 99.3% tive	lication US/08233 17 TION: OTAN, James L. ay, William W. Ollinson, Karen S. OLLINGES: EADDRESS: Seed and Berry OC Columbia Centee hington S.A. T.S.A.	1536 2 1536 2 1536 2 1536 2 1536 2 1026 1 1026 1 211 2 211 2 2 2 2
; Score ; Pred. 0; Mi	3788 S. C. C. C. C. P. C.	US-08-5 US-08-7 US-08-7 US-08-7 US-08-1 US-08-1 US-08-1 US-08-1 US-08-3 US-08-3 US-08-3 US-08-3 US-08-3 US-08-3
768; No. 8. smatche	OMPOSI 01 Fif 01 Fif 88A	-08-530-198-2 -08-469-880-2 -08-728-470-2 -08-617-697-2 -08-194-290-7 -08-1614-377A-7 -09-142-648B-7 -08-32-730A-16 -08-32-730A-16 -08-387-874-16 -08-383-619-16 -08-383-619-16 -08-383-619-16 -08-383-619-16 -08-383-619-16
DB 1; 3e-68; 3 1;	enu FO	-2 -2 -2 -2 -2 -2 -2 -2 -2 -3 -3 -16 -16 -16 -16 -16
Length 1 Indels	e e	
151; .s 0;	ON .	Sequence Sequence
Gaps		2, Appli 2, Appli 2, Appli 2, Appli 2, Appli 3, Appli 7, Appli 16, Appl 16, Appl 16, Appl 16, Appl 16, Appl 16, Appl 16, Appl
0;		

B

MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

60

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                 RESULT 3
US-08-864-038A-3
; Sequence 3, Application US/08864038A
; Patent No. 6001592
                                                                                                                                        δõ
                                                                                                                                                                      Вþ
                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-233-788A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                           В
                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: US-08-233-788A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-08-222
Sequence 57, App. 56356
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 112; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                         APPLICATION NUMBER: FILING DATE: 26-APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300 (CITY: Seattle
                                                                                                                                                                                        22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                        VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRY: U.S.A.
98104-7092
                                                                                                                                                                                                                                                                                                                                      120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08233788A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collinson, Karen S. Clouthier, Sharon C.
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1994
                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                        SEEDANBERRY ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHODS AND COMPOSITIONS FOR DETECTION OF SALMONELLA
                                                                                                                                                                                                                                                 76.1%; Score 588; DB 1; 100.0%; Pred. No. 2.3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/233,788A
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920043.403C2
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #1
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                              Length 120
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                    Gaps
```

Qy 밁 δõ 밁 Qy

US-09-336-447A-5

Sequence 5, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION:

APPLICANT: HANSEN, APPLICANT: AEBI, C

AEBI, CHRISTOPH COPE, LESLIE D. MACIVER,

ERIC J.

APPLICANT:

```
US-08-864-038A-3
RESULT 4
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 8-
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,31
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KUNIO NAPPLICANT: KUNIO NAPPLICANTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1 FILING DATE: May 28, PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                       504 LGGGSAAAAAAAAAAASGGGGRALRRALRRQMRGGGSAAA 543
                                                                                                                                                                                                         419 LLKSSASASASASASASAG-----GGGGGGGNGGGNGGGG------GGGAGALA---- 460
                                                                                         118 YGGNNAALVNQTASDSS-----VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: Microsc SOFTWARE: Word Perfect 6.
                                                                                                                                                                                                                                                                                                                                                                              LOCATION: from 1 to 738 IDENTIFICATION METHOD: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL TYPE: mantle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                   63 ARKSETTITQSGYGNGADVGQGADNSTIELTQ----NGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: peptide LOCATION: from 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                           3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514-01
                                                                                                                                 ---AALAAAGAGGGLGGGGGGGALAAALAAAGAGGGGFGGLGGL-
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsu-city
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mie-prefecture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isshinden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunio NAKASHIMA et al.

VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212)953-7733
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Word Perfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pinctada fucata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        812-5 Hirano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-July-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsoft Windows
                                                                                                                                                                                                                                                                                                      12.6%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP 8-184459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/864,038A
, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.50 inch, 1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                  H
                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                (by experiment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F-5610
                                                                                                                                                                                                                                                                                                      Score 97.5; DB Pred. No. 0.16;
                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
                                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                                          ω
••
                                                                                                                                                                                                                                                                                                                          Length 738;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                        49;
                                                                                                                                     င်္ပ
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                     503
                                                                                                                                                                                                                                                                                        9
```

```
RESULT 5
US-09-196-387-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-336-447A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09196387 Patent No. 6277613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/336,447A CURRENT FILING DATE: 1999-06-21 NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 892
TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,38
                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
           SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRE1 AND METHODS TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: de Lange, Ti
APPLICANT: Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
                                                        TELEFAX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 HNQATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 GGGNHN------GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY--- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NOTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATGNNSTVAGGS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GNGADVGQGADNSTI--ELTQNGFRNNATIDQWNAKNSDITVGQYG---GNNAALV--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDTN-----DANGTYSTIGGGYYSRA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hackensack
New Jersey
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FREDENBURG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 Hackensack Avenue, 4th Floor
                                                                                        201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Lange, Titia
                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSS A.
                                                                                                                                                                                                                                                                                                                        US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 94; DB 4
Pred. No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
```

```
δÃ
                                                                     밁
                                                                                                   δδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: US-09-196-387-8
                                                                                                                                                                                                         US-09-196-387-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-196-387-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 627761
                                                                                                                                     Matches
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/0 FILING DATE: June 10, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: de Lan
APPLICANT: Smith,
158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                            TELEX: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 35; Conserv
                                                                                                                                     Local Similarity
es 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                   VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09196387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 Hackensack Avenue,
                                                                                                                                                                                                                                                                                                                                            201-343-1684
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Lange, Titia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klauber & Jackson
                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Susan
                                                                                                                                                   11.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A PROTEIN THAT BINDS TO TRF1 AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09/095,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92; DB Pred. No. 0.5;
                                                                                                                                                   Score 92; DB 4
Pred. No. 0.77;
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4th Floor
                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 673;
                                                                                                                                     57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Indels
                                                                                                                                                                   Length 949;
                                                                                                                                     Indels
                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                     157
                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
```

us-09-196-387-2

Sequence 2, Application US/09196387 Patent No. 6277613

GENERAL INFORMATION: APPLICANT: de Lan APPLICANT: Smith,

Smith, Susan

A PROTEIN THAT BINDS TO TRF1 AND METHODS

de Lange, Titia

RESULT

```
; MOLECULE TYPE:
; HYPOTHETICAL:
US-09-196-387-2
                                                                                                                                                                        RESULT 8
US-09-336-447A-13
                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                   Вb
                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                        GENERAL INFORMATION:
                                                                                                                                       Sequence 13, Application US/09336447A Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                   APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A PROTECTION OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/0 FILING DATE: June 10, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                                                 99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                  6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09/095,225
                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB 4; Length 1327; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

Local Similarity hes 39; Conserv

Conservative

Mismatches

54;

Indels

50;

Gaps

7;

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Moraxella catarrhalis US-09-336-447A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-056-556-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 204, Application US/09056556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                     TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 N-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 NAALVNOTASDSSYMVROVGFG-NNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LLIVGILGMATTASAQQTIARQ--GKGMHSIIGGGNDNEANGDYSTVSGGDYNEA----
                                                                                                                                                                                                                        NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 07-API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                  STRANDEDNESS:
                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                  OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKVAAFAAIVVSGSALAGVVPQWGGGGNHN--GGGNSSGPDSTLSIYQYGSANAALALQS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KGDSSTIGGGYYNEAN----GDSSTI----GGGFYN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98104-7092
                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NSATGMYSTIGGGDNNSATGRY 150
                                                                  linear
                                                                                                                                                                                         (206)
                                                                                                                                                                                                                                                                                                                07-APR-1998
                                                                                                                                                                       682-6031
                                                                                                                                                                                           622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.6%; Score 89.5; D
26.5%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOUNDS AND METHODS FOR THE PREVENTION AND
11.5%;
25.3%;
                                                                                                                                                                                                                                                                                                                                us/09/056,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Mismatches
                                                                                                                                                                                                                             210121.457
 Score 89; I
                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                   Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·EAKGESSTIG - -GGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
```

TRE

```
₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 941
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                            US-08-808-599A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-336-447A-9
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                          Dequence 24, Application US/08808599A Patent No. 6111089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.5%; Score 81.5; DB 4; Length 941; Best Local Similarity 26.4%; Pred. No. 8.1; Matches 43; Conservative 13; Mismatches 68; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09336447A Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/336,447A CURRENT FILING DATE: 1999-06-21 NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOF
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                 ADDRESSEE: Campbell
                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 QAKGEHSTIA--GGKN----NQATGNGSF---AAGVENKADAN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 NAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 TVGGGFTNEAMGEYSTVAGGANNQAKGNYSTVGGGNGNKAI------GNNSTVVGGSNN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 GTGNSGLENSGTNNVGIFNAGTGNVGIANSGTGN 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464
                                                                                                                          STREET: 4370 La JC
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 DARKSETTITQSGY-----GNGADVGQGADNSTIELTQNGFRNNATI---DQW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 AQVVKTNNKKNGTHPFIGGGDYNTTKGNYPTIGGGHFNTAEGNYSTVGGGFTNEAIGKNS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
  OPERATING SYSTEM:
                         COMPUTER:
                                                                                           ZIP: 92122
                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAIVVSGSALAGVVPQWGGG-----GNHN--GGGNSSGPDSTLSIYQYGSANAALALQS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFGNAGDFNQGFANT------GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN------ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEBI, CHRISTOPH
COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISKE, MICHAEL J.
                                                                                                                                                                          E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                       Fukuda, Michiko N.
                                                                                                             USA
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            Trophinin, Trophinin-Assisting
Proteins and Methods to Inhibit Implantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-804-227C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-808-599A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08804227C Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DeHoff, Bradley S.
APPLICANT: Kubstoss, Stuart A.
APPLICANT: Rostock, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/317,522 FILING DATE: 04-OCT-1994 PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1160 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 NFGGALNNSAGFGGAMNTSASFGGVLNNSAGFGGAINTSAN 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515 AISTSFSGVLNSSASFGGAIN----TSAGFGSTLN----SSASFGSALSTSASFGGVLN 565
                                                                                                                                                                                                                                            COUNTRY:
ZIP: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 QYGG--NNAA----LVNQTASDSSVMVRQVGFGN--NATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    566 GRAGFGGALNT-----NATFGGVLNGSAGFGGAMNTNATFG--GALNSNAGFGGAISTST 618
                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                  STREET: LILLY CORP
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 28-FEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 TQSGYGNGADVGQGADNSTIELTQNG-----FRNNATIDQWNAKNSDITVG------ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 28.0 es 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                              46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                          LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1160 amino acids
                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/439,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/808,599A
                                                                                                     US/08/804,227C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 81; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Length 1160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
```

```
Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           рЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-737-716-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-804-227C-3
                                              ; MOLECULE TYPE: US-08-737-716-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08737716 Patent No. 5955258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                          APPLICATION NUMBER: EP FILING DATE: 12-MAY-19: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           FILING DATE: 12-MAY-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                       SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           482 AQAARLYDALTGTGTGQGAGQGAGPGTAEVAGALAHARTAFRHRAVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 VSSFGASGINAHVVLESVPAGEPPAAGRPEDIGGAWIVSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 VGQYGGNNAALV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 10.5%;
Local Similarity 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDARKSETTITQSGYGNGADVGQGADNSTIEL-----TQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/OFILING DATE: 22-APR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VAAFAAI-----VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                              TOPOLOGY:
                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LGGNRAELL 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                          20005-3918
                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1864 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Pillsbury Madison & Sutro, L.L.P. 1100 New York Avenue, N.W.
                                                                                                              437 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adrianus Marinus LEDEBOER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jan KOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerard VENEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Girbe BUIST
                                                                                  linear
                                                               protein
                                                                                                                                                             12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Process for the lysis of a culture of lactic acid bacteria by means of a lysin, and uses of the resulting lysed culture.
 10.4%;
                                                                                                                                                                              EP 94201353.3
                                                                                                                                                                                                                             PCT/NL95/00170
                                                                                                                                                                                                                                                                                           US/08/737,716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-8231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 81; DE
Pred. No. 22;
 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
 80.5; DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Indels
                  2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1864;
                  Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---RGPAALR 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
```

```
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ър
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Helicobacter pylori US-09-043-123-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-043-123-2
                                                                                                                                                                                                                                                                                            QY
                                                                                                                                                                                                                                                                                                                                 Вр
                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ωy
                                                                                                                                                                                        RESULT 15
US-08-209-747-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09043123A Patent No. 6096521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                   Sequence 8, Application US/08209747 Patent No. 5733771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MEYER, Thomas F.
APPLICANT: BLUM, Andre
APPLICANT: CORTHESY-THEULAZ, Irene
TITLE OF INVENTION: NEW ADHESIN FROM HELICOBACTER PYLORI
FILE REFERENCE: 05648004
                                             GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: cDNAs Encoding
TITLE OF INVENTION: Silk Proteins
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/043,123A CURRENT FILING DATE: 1998-06-26 EARLIER APPLICATION NUMBER: DE/195 35 321.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HAAS, Rainer APPLICANT: ODENBREIT, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1995-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 GASLNRIISQYNLTRFDGASSAGNTNSGGSTTTITNNNSGTNSSSTTYTVKSGDTLWGIS 257
                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 -PSTGSGSTATNN 382
                                                                                                                                                                                                                                                             346 SSQVNAFNGFITKIGYKQFFGENKNVGLRYYGFFSYNGAGVGNGPTYNQ 394
                                                                                                                                                                                                                                                                                                                                                                                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                123 AALVNQ--
                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                       29
STREET:
                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QNG-----FRNN-ATIDQWNAKNSD-ITVGQYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRYGISVAQIQSANNLKSTIIYIGQKLVLTGSASSTNSGGSNNSASTTPTTSVTPAKPTS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSALAGYVPQW-----GGGGNHNGGG-----NSSGPDSTLSIYQYGSANA----- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTTVKVKSGDTLWALSVKYKTSIAQLKSWNHLSSDTIYIGQ-----NLIVSQSAAASN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ALALQSDARKSETTITQSGY-----GNGADVGQGADNSTIELT-----
                                                                                                                                                                                                                                                                                                                                                                  ETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDIT----VGQYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                    GPSGDSGAAAAFLDAALAQHVFNSANAGNDLSAKEFTSLVQNIVNNSQNALTLANNANIS 293
                                                                                                                                                                                                                                                                                                                               NSTGYQVSYGGNID--QARSTQLLNNTTN-----TLAKVSALNNELKANPWLGNFAAGN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                     GGNHNGGGNSSGPDSTLSIYQYGSANA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518
P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Birch, Stewart, Kolasch & Birch
O. Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.4%;
                                                                                  cDNAs Encoding
                                                                                                                                                                                                                                                                                                    ---TASDSSVMVRQVGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 80.5; DI
; Pred. No. 4.7;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                     Minor Ampullate Spider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                    --GNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ALALQSDARKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
```

```
CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 2040-3487

COUNTRY: USA

ZIP: 2040-3487

COUNTRY: LSM PC COMPACIBLE

COMPUTER READABLE FORM:
MEDIUM TYRE: F10ppy disk
COMPUTER READABLE FORM:
MEDIUM TYRE: F10ppy disk
COMPUTER READABLE FORM:
MEDIUM TYRE: F10ppy disk
COMPUTER READABLE FORM:

MEDIUM TYRE: 14 MAR-1994

CLASSIFICATION NUMBER: US-/08/209,747

FILING DATE: 14 MAR-1994

CLASSIFICATION: 530

APPLICATION NUMBER: 1447-104P

FELEPHONE: 703-205-8000

TROMMENTION FOR SED IN NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTE
```

#### THIS PAGE BLANK (USPTO)

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
     564.5
1112.5
1112.5
1112.5
1112.5
1111.5
1110.5
1105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
105.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-543-407-5
773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             October 11, 2002, 21:10:53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283138 seqs, 96089334 residues
100.0
100.0
75.8
73.0
73.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
DB
                                                                      D90806
D95965
E95965
E959667
C970787
C797087
C85665
C8566604
AHC6040
AHC6040
AHC6040
AHC6040
AHC6040
AHC6040
AHC6040
AHC6040
C842136
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Search time 20 Seconds
(without alignments)
725.474 Million cell updates/sec
                                                                                                                                                                                 probable PPE prote
probable PPE prote
F3F19.21 protein
ice nucleation pro
                                                                                                                                                                                                                                                                                                   cnjB protein
probable PPE
                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical prote hypothetical glyci
                                 probable PPE prote nuclear pore compl
                                                                      probable PPE prote
protein kinase sgg
                                                                                                        DNA-binding protei ovo protein - frui
                                                                                                                                               probable PPE prote probable PPE prote
                                                                                                                                                                                                                                                              hypothetical prote conserved hypothet
                                                                                                                                                                                                                                                                                                                                       nucleation compone
                                                                                                                                                                                                                                                                                                                                                                              curlin minor chain
                                                                                                                                                                                                                                                                                                                                                                                                minor curlin subun
                                                                                                                                                                                                                                                                                                                                                                                                                 curlin nucleator p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           curlin major subun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          curlin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                major curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                            fimbrin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fimbrin protein
                   nucleation act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .,
                                                                                                                                                                                                                                                                                                   prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            csg
                                                                                                                                                                                                                                                                                                                       Tet
```

A; Molecule type: protein A; Residues: 21-52 <CO2>

A; Molecule type: DNA A; Residues: 1-151 <COL>

A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 A;Accession: PC6015

4. 4 5. 4	43	41 42	40	39	38	37	36	35	34	33	32	31	30
89.5	91 91	91.5 91	91.5	92	92	92.5	92.5	93	93.5	93.5	93.5	94	95.5
11.6	11.8	11.8 11.8	11.8	11.9	11.9	12.0	12.0	12.0	12.1	12.1	12.1	12.2	12.4
262	141	745 141	256	1655	409	1651	1317	586	1322	1238	447	652	1258
2 4	) N	N N	N	Ŋ	N	N	N	2	2	2	N	N	Ν
S00275	AB3143	E64559 B98145	T03371	E97835	T20847	JC1340	A54831	T26667	S07053	AH0038	G84687	E97857	JQ0188
nypothetical glyc tail fiber protei	hypothetical	outer membrane pro hypothetical prote	glycine-rich prote	hypothetical prote	hypothetica	outer membrane pro	nuclear pore comp	hypothetical prote	ice nucleation pro	probable exported	probable disease	cell surface antig	ice nucleation pro

C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 08-Oct-1999
C;Accession: JC6039; PC6015; A44898
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996

fimbrin protein agfA precursor -

Salmonella enteritidis

A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039; MUID:96146512 A;Accession: JC6039

prote A;Experimental source: strain 27655-3b

A;Note: the authors translated the codon ACG for residue 44 as Ile
R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.

J. Bacteriol. 173, 4773-4781, 1991

A;Title: Purification and characterization of thin, aggregative fimbriae from Salmone
A;Reference number: A44898; MUID:91310586
A;Contents: 27655 ρ В A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue p. C;Keywords: fimbria δÃ В Qy F;1-20/Domain: signal sequence \*status predicted <SIG> F;21-151/Product: fimbrin protein agfA \*status experimental <MAT> C; Function: A;Gene: agfA C; Genetics: A; Note: sequence extracted from NCBI backbone (NCBIP: 45936) A; Molecule type: protein A; Residues: 21-33 <CO3> A; Status: preliminary A; Accession: A44898 Matches Query Match Best Local Similarity 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 61 61 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120 100.0%; Score 773; DB 2; ilarity 100.0%; Pred. No. 4.3e-56; Conservative 0; Mismatches 0; 151 Length 151; Indels plasminogen activator 0 Gaps 120 0

```
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 199 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is
A;Reference number: S70783; MUID:96414468
A;Accession: S70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , S.; Moule, S.; O'Gaora, Nature 413, 848-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          major curlin chain precursor [imported] - Salmonella enter C;Species: Salmonella enterica subsp. enterica serovar Typi A;Note: this species has also been called Salmonella typin C;Date: 09-Nov-2001 *sequence_revision 09-Nov-2001 *text_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hanmar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                          Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Experimental source: strain K12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
C;Aaccession: S70788; G64846; S31202; S34560; S34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     curlin protein csgA precursor - Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-151 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: AI0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd
                                                                                                  A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
                                                                                                                                                    A;Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-151 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001,Accession: AI0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGUHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAALVNQTASDSSVMVRQVGFGNNATANQY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Gaora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             csgA protein; major curlin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 773; DB 2;
Pred. No. 4.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterica serovar Typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enterica subsp. enterica
                                                                                                                                                    translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                 coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                       not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dowd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.; Wain, J.; Churcher, L.; White, N.; Farrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibronectin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                             PID: 91787279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stevens, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serovar
                                                                                                                                                                                                                                                                                                                                    1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              გ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
```

```
A; Molecule type:
A; Residues: 21-42
R; Olsen, A.N.; Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The RpoS sigma factor relieves H-NS-mediated A;Reference number: S31202; MUID:93211294 A;Accession: S31202
                                                                                                                                                            curlin major subunit CsgA [imported] - C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: major component of wild-type curli; interaction between A;Note: curli are thin, coiled fibers expressed on the surface of Esch and H-kininogen; in the absence of CsgA, CsgB can self-assemble into F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Restdues: 1-133,'RQRDSGWLW' <OLS3>
A;CEXPERIENCES: EMBL:LO4979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S34559
A; Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:L04979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-6,'V',8-151 <OLS1>
                   DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: csgA
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S34560
A; Status: preliminary
                                                                                                    gasawara, N.;
                                                                                                                       R; Hayashi, T.;
                                                                                                                                                 C; Accession: D90806
                                                                                                                                                                                                                                  D90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tocal Sir
tes 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.N.; Arnqvist,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                     GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                                                                                   TDARNSDLTITQHGGGNGADYGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type: protein
21-42;44-50 <OLS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                        Yasunaga,
                                                                                                                       Makino, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                    K.; Ohnishi, M.; Kurokawa, K.; Ishii
T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.8%;
74.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 586; DB 2
Pred. No. 7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                     18-Jul-2001 #text_change
                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:AAA23616.1; PID:g290425
W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                              coli (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interaction between CsgA and CsgB the surface of Escherichia coli th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                            Ishii, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcriptional
                                                                                                          3
                                                                                                        Shinagawa,
                                                                                                                                                                       18-Jul-2001
                                                                                                                                                                                                              O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                            Yokoyama,
                                                                 coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repression
                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                          ۳.×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0f
                                                                                                                                                                                                                   RI
```

```
QΥ
                                  Дb
                                                                Qγ
                                                                                                                                                                                         A; Experimental source: C; Genetics:
                                                                                                                                                                                                       A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-152 <HAY>
                                                                                                                                                                       A; Gene:
                                                                                                      Matches
                                                                                                                                       Query Match
   60
                                                                                                                        Local
                                                                                                                                                                           ECs1420
QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
                                                    MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                  MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
                                                                                                                      Similarity
                                                                                                      Conservative
                                                                                                                      73.0%;
73.0%;
                                                                                                      20;
                                                                                                                      Score 564.5; DB 2
Pred. No. 3.9e-39;
                                                                                                      Mismatches
                                                                                                                                        2
                                                                                                        Indels
                                                                                                      1.
                                                                                                      Gaps
                                     60
                                                                                                        ۲.
```

•

```
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium mellioti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                              C;Accession: E95965
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) maga
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-152 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iller, L.; Grotbeck, E.J. Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                          A; Gene:
                                                                  A; Contents: annotation
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-2174 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical
                                          Genetics:
                                                                                                                                                                                                                                                                                                                                            Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                          SMb21548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              csgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL•60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.0%;
73.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 564.5; DB 2
Pred. No. 3.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vorholter, F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSPDB:GN00145; UWGP:Z16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        the N2-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.J.;
K.; A[
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apodaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hernai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mayher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDL93
                                                                                                                                                                                                                                                                                                                                                                                                           endo
                                                                                                          밁
                                                                                                                                              Qy
                                                                                                                                                                                            8
                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
C90806
minor curlin
```

```
curlin nucleator protein csgB precursor - Escherichia coli
% Alternate names: csgB protein; curlin nucleation component; mi
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
C;Accession: S70787; F64846
R;Hammar M: Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for productio
A;Reference number: S70783; MUID:96414468
A;Accession: S70787
                                                                                                                                                                                                                                                                         A;Description: minor component of wild-type curli; interaction between CsgA and A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia co and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia A; Reference number: A64720; MUID:97426617
A; Accession: F64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563 A;Experimental source: strain K12, substrain W3110 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augu R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S70787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-151 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g17872A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local s
Matches 40
                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794
  77
                                                                                                                                       38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                              98
                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                   csgB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGGNGGAGGEVSVSLTDSAIRTGQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIATAGAGAVGILAQSIGGGGGN~~~GGNATGGDAGFGSFQIGGGGGG-~~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
                                         RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                        AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                                       SSGPDSTLSTYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQYGGNNAA--LVNQTASDSSVMVRQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GGYANTANVGFKGLTLTTQGSHAAGIVAQSVGGGGGTGGTASSYSAGIGFTASVAV 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITQSGYGNGADVG------QGADNSTI--ELTQNGFRNNATIDQWNAK---NSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conser
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             23.15
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                            14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.6%;
                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 113; DB Pred. No. 0.4;
                                                                                                                                                                                                       Score 112.5; DE Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141
                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2,
                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli K-12
                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not show
                                                                                                                                                                                                                                    151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            minor curlin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-Jul-2000
                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of,
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibronectin-
                                                                                        76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             August
                                                                                                                                                                                   Ŋ
                                                                                                                                                                                                                                                                                                                                                   and CsgB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995
еу, м.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
```

subunit precursor CsgB [imported]

Escherichia

coli (strain O157:H7,

us

```
gasawara, N.; Yasunaga, T.; Numaru, C., Sasawara, N.; Yasunaga, T.; Numaru, C., Sasawara, N.; Yasunaga, T.; Numaru, C., Sawara, 
fimbrin protein agfB precursor - Salmonella enteritidis (;Species: Salmonella enteritidis C;Species: Salmonella enteritidis C;Species: Jobec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 C;Accession: JC6040 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996 A;Bacteriol. 178, 662-667, 1996 A;Reference number: JC6039; MUID:96146512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
R; Hayashi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequen
                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-151 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glas: iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-151 <HAY>
                                                                                                                                                                                                                                                                           JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  csgB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECs1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNNATIDQWNAKNSDITYGQYGGNNAALVNQTASDSSYMYRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSYMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . . . . . . . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                            SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Makino, K.; Ohnishi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 112.5; DE Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 112.5; DB Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurokawa, K.;
Shiba, T.; Hat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ishii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glasner,
anta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         × . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.D.; Rose, Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yokoyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
                                             fimbriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Han,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
G
```

```
nucleation component of curlin monomers [imported] - Salmonella enterica subsp. c;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 c;Accession: AH0635 R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Cth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; S.; Moule, S.; O'Gaora, P.
                                                                                          cnjB protein - Tetrahymena thermophila c;Specles: Tetrahymena thermophila C;Date: 19-Mar-1997 #sequence_revision C;Accession: S42136; S42135; S03650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: minor of A:Note: fimbriae bind
                                                                                                                                                                        RESULT
S42136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-151 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , S.; Moule, S.; O'Gaora, Nature 413, 848-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: fimbria
F; 1-21/Domain: signal sequence #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713 A;Experimental source: strain 276755-3b
A; Reference number:
A; Accession: S42136
A; Molecule type: DNF
                                                                                                                                                                                                                                                                                      QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics
A; Gene: ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Authors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: JC6040
                                      submitted to the EMBL Data A; Reference number: S42136
                                                                                                                                                                                                                                                    Дď
                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                QV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: AB0502; A; Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;22-151/Product: fimbrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                            R; Taylor, F.M.; Martindale, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 EGGNNKAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                          95
                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                  51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STY1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSANAALALQSDARKSE-----TITITQSGYGNGADVGQ-GADNST--------IELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                                                                                                                                                                                  EGENNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                      NGFRNNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGFRNNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-151 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  component of thin aggregative d to fibronectin, plasminogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                           14.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                        Library,
                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111.5; DB Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agfB
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 111.5; DB Pred. No. 0.027;
                                                        October 1992
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted <SIG>
#status predict
                                                                                                                  18-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Χ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simmonds, M.;
drug resistant
                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fimbriae
tissue plasminogen
                                                                                                                #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skelton, J.;
Salmonella e
                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activator
                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e, N.; Farr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stevens,
                                                                                                                                                                                                                                                                                                                                                                                                           ហ
•-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enter
```

```
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-645 <COL>
A;Cross-references: GB:AL021958; GB:AL123456; NID:g3261536; PIDN:CAA17522.1;
A;Experimental source: strain H37Rv
A;Experimental source: strain H37Rv
                                                                                                                                                                                       Connor, R.; Davies, R.; Devlin, K.; Feltwell, T. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, Nature 393, 537-544, 1998
A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Decliphering the biology of Mycobacterium A:Reference number: A70500; MUID:98295987
A:Accession: F70825
                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hornis, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:1451-1464/Region: zinc finger CCHC F:1478-1491/Region: zinc finger CCHC F:1501-1514/Region: zinc finger CCHC F:1530-1543/Region: zinc finger CCHC F:1530-1543/Region: zinc finger CCHC F:1530-1563/Region: zinc finger CCHC F:1579-1592/Region: zinc finger CCHC F:1602-1615/Region: zinc finger CCHC F:1602-1615/Region: zinc finger CCHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene
A;Reference number: S03650; MUID:88189811
A;Accession: S03650
  A;Gene: PPE
C;Superfamily:
                                               A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jan-2000
C;Accession: F70825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1164-1450/Region: glycine-rich
F;1451-1464/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Genetic code: SGC5
A;Introns: 85/3; 136/1;
C;Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A: Residues: 236-250, 'I', 252-255, 'N', 257-773
A: Cross-references: EMBL: X06462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343
A; Cross-references: EMBL:L03710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and
A;Reference number: S42135; MUID:94051569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: cnjB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-1748 <TAY>
A; Cross-references: EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1626-1748/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1723 WGSNNQAS 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1640 QFGGGGNSNGGQSWGTSSGSDWN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 FGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV•81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SGSGNQ----TGGGWGSN---DNQQQQNENTGGGGWGSSNS----NQTNNESS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F.M.;
unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martindale,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136/1; 157/3; 201/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: L03710;
  collagens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 108; DB Pred. No. 0.8; 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g161751; PID:g161752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 motiff
motiff
motiff
motiff
motiff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycine-rich repeats in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CQSNVQES-TTTSSGGWGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                   Whitehead, S.; Barrell, B.G. tuberculosis from the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499/1; 573/2; 607/3; 708/3; 777/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Tetrahymena thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1680
                                                                                                                                                                                                                                                                                                                            Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded
                                                                                           PID:e125329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                   genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ьy
                                                                                                                                                                                                                                                                                                                                 S
```

```
conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AD3143 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
H98144
                                                     A;Title: The Genome of the Natural Genetic A;Reference number: ABZ577; PMID:11743193 A;Accession: AD3143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A97359; PMID:11743194
A;Accession: H98144
A;Status: narrivitation:
                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
A; Molecule type: DNA
A; Residues: 1-145 < KUR>
                                      A;Status: preliminary
                                                                                                                    ster, E.W.
                                                                                                                                    Science 294, 2317-2: A; Authors: Yoo, H.;
                                                                                                                                                                                                                                                                                                                 AD3143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-145 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Goodner, B.; Hinkle, G.; G.
A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: H98144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dβ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                             Karp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70
                                                                                                                                P.; Romero, P.; Zhang, S.
294, 2317-2323, 2001
295: Yoo, H.; Tao, Y.; Biddle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGR_L_228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---GNNAALVNQTASDS-----SVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLKVAAFAAIVVSGSALAGVVPQWGG-----GGNHNGGGNSSGPDSTLSIYQYGSANA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNTGNNNIGIGLTGSNQIGFGGLNSGSGNIGFGNSGTGN 384
                                                                                                                                                                                                                                                                                                                                                                                             GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                               GQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYNR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTPGNGNVGIGNGGNGNFGGGNT-----GNANIGLGNVGDGNVGFGNSGSYNFGF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGNGNVGIGPSSFNVGSGNIGNANVGGGNSG-DNNFGFGNFGNANIGIGNAGPNMSSPAV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSALAGVVPQ-----WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITQS----GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB:AE007870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G.; Gattung, S.; Miller, N.; E
C.; Allinger, M.; Doughty, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -HQYGRHNLSAVGQEGHDNYGSTTQNGNRNVAGI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107.5; DE 
Pred. No. 0.29; 
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAK88682.1; PID:g15158413; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105.5; D. Pred. No. 0.08;
                                                                                                                              P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-Oct-2001 #text_change 11-Jan-2002
                                                                                             Engineer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biotechnology Agent Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blanchard, M.; Qurollo, Scott, C.; Lappas, C.;
                                                                                               Agrobacterium tumefaciens C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Markelz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B.; Goldm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            င္ပ
```

GB:AE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187

```
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4768
A;Gene:
```

```
RESULT 15
Q98LN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A CONTRACTOR OF THE CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                              용
                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ફ
Search completed: October 11, 2002, 21:14:22 Job time : 30 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.0%; Score 100.5; Best Local Similarity 25.3%; Pred. No. 68; Matches 42; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q98LN6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-MAFF303099;

MEDLINE-21082930; PubMed-11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic bacterium

Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

EMBL: AP002996; BAB48427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 3659 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
MLL0950 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::|::: | |:
184 NVMMNKSPTQSFVV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AALVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 QG-----STTVVLNNHGFSGNAVNVPEMPVHNSYGAPPQGAQQIPVSQMSVNP 183
                                                                                                                                                                                                                                                                                                                                                                                                                     375 GNNSQGILAQTIGGGGGDGGSNFGLFASGGS---GSLG-GNGGPAN 416
                                                                                                                                                                                                                   107 NAKNSDI---TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                 323 IYSHGIAAQSIGGGGGSAGGFGLFSSSGGSG---GNGGNGGIVQVT-----NNANIATW 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGYGNGADVGQGADNSTIELTQNGFRNNA-TIDQWNAKNS------DITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                                                                   IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337498 MW; 7B7BC7EC5C0F3816 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 3659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

```
RESULT 12
P71868
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                     ρ
                                                                                                                                                            Вþ
                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 40
                                                                      Q9KKB1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandraam M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
Nature 393:537-544(1998).
EMBL; 282098; CAB05045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Cr
01-FEB-1997 (TrEMBLrel. 02, La
01-DEC-2001 (TrEMBLrel. 19, La
01-DEC-2001 (TrEMBLrel. 19, La
                            01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01469; Pentapeptide_2; 10.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RV3533C OR MTCY03C7.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P71868;
01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P71868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                  OMPB
                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002989; Mycobact_pentapep
InterPro; IPR000030; PPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 GTLN 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146
                                                                                                                                                            293
                                                                                                                                                                                                                    233
                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNA-----GFFN---MGIGNAGNEDMGVGNGGSFNVGVGN--AGNQS-----VGFGNA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN
                                                                                                                                                                                                                                                                                                       VPQWGGG--GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
               (FRAGMENT).
                                                                                                                                                            IGAGNTGSSNWGFGNNGIGN 312
                                                                                                                                                                                                                                                                            LPNLGIGNIGNANLGGGNTG-DLNTGNGNIGNINLGSGNRGDANLGSGNIGNSNVG-GGN 232
                                                                                                                                                                                       ---SSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                    VGNGNFGSGNGRAGLPGSGNVGNGNLGNSNLGSGNTGNSNVGFGNTGNNNVGTGNAGSGN 292
                                                                                                                                                                                                                                               VGQ---GADNSTIEL----TQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASD 132
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
                                                                                                                                                                                                                                                                                                                                                                                             il protein; Complete proteome.
582 AA; 55503 MW; B895BDD55979A9C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                       PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                 13.5%;
                               15,
                                                                                                                                                                                                                                                                                                                                  ; Score 104.5;
; Pred. No. 4.6;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
                                                                                       1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           582 AA
                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                  DB 16;
                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                             6;
```

```
Q9SAF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
Best Local
                                                        Submitted (MAY-1999) to the EEMBL; AC007357; AAD31072.1; -
InterPro; IPR000504; RRM.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                         STRAIN-CV. COLUMBIA;

Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Len:
Vysotskaia V.S., Schwartz J.R., Luros J., Ngan I., Gonzalez A.,

Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A.,

Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,

Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walk,

Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome 1 BAC F3F19 sequence.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene coding the outer-membrane protein rOmpB (ompB). Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000). EMBL; AF123713; AAF34116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia japonica.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9SAF2;
01-mAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003858; rOmpA_rOmpB. pfam; pF02708; rOmpA_rOmpB; 1. NON_TER 1618 1618 AA; 164193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20393643; PubMed=10939649;
Roux V., Raoult D.;
"Phylogenetic analysis of members of the genus Rickettsia"
                                                                                                                                                                                                                                                                                                                                                                               eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                         F3F19.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9SAF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        F3F19.21 PROTEIN.
                                            SEQUENCE
                                                                                                                                                 Theologis
                                                                                                                                                                  STRAIN=CV.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       571 LTNAQTLTISGTIGIIGANNTTLGQFNIGSSKTTLNGGNVAINELVIGNNGS 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QWNAKNSDI--TVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TLTLGGANIISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQTGVVDASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SETTITQSG----YGNGADVGQGADNSTIELTQNGFRNNATID------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLAAGAITLDGSATI-----TGDIGNGGG--
 Similarity
                                            573 AA;
                                                                                                                                                                  COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                               Brassicales;
                                             61400 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%;
 13.2%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                 Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103; D
Pred. No. 18;
                                                                                                                                    EMBL/GenBank/DDBJ databases
 Score
Pred.
                                             0D1C10384B86C2BC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66AD2199620750C6 CRC64;
   102;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  573
    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
 DB
.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1618;
                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GAALQSITLANDATK 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                  573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                             Walker
                                                                                                                                                                                                                                                                                                        Lenz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                        c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
```

```
Q9S3J8
ID Q9
AC Q9
DT Q1
DT Q1
DE C1
CN C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멁
                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O53818 PRELIMINARY;
O53818;
O1-JUN-1998 (TrEMBLrel. 0
O1-JUN-1998 (TrEMBLrel. 0
O1-DEC-2001 (TrEMBLrel. 1
                                                                           Q9S3J8;
Q9S3J8;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RV0755C OR MTV041.29.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1723
CSGB. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TubercuList; Rv0755c; Interpro; IPR002989; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 393:537-544(1998).
EMBL; AL021958; CAA17522.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98295987; PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPE-FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 645 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000030;
                                                                                                                                                                                                                                                                                                                 346
                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                     296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGSNNQAS 1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SGSGNQ----TGGGWGSN---DNQQQQNENTGGGGWGSSNS---NQTNNESS---
                                                                                                                                                                                                                                                                                                                 GNTGNNNIGIGLTGSNQIGFGGLNSGSGNIGFGNSGTGN 384
                                                                                                                                                                                                                                                                                                                                                                  ---GNNAALVNQTASDS-----SVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITQS----GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGNGNVGIGPSSFNVGSGNIGNANVGGGNSG-DNNFGFGNFGNANIGIGNAGPNMSSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSALAGVVPQ-----WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                                                                                                                                                                                                                  PTPGNGNVGIGNGGNGNFGGGNT------GNANIGLGNVGDGNVGFGNSGSYNFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01469; Pentapeptide_2; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645 AA;
                                                                              (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence up
(TremBLrel. 16, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                  PRELIMINARY;
                                                        PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62693 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobact_pentapep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19,
                                                        (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107.5;
Pred. No. 3.1
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348FF4265DFE15FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645
                                                                                                                                                                                  91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                  ĄΑ
                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length
                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
```

```
ALCONDARY OF THE STANDARY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
밁
                                          QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 28
                                                                                                                     Query Match
Best Local
                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 01-JUN-1998 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078:K80 isolates associated with
"Si inserti on in csgB and reduced persistence in poultry infection."
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPE_FAMILY PROTEIN.
RV3159C OR MTV014.03C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             053309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKANSPOSON=INSERTION SEQUENCE IS1;
MEDLINE-99314153; PubMed-10386375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                Complete proteome. SEQUENCE 590 AA;
                                                                                                                                                                                                                                                                                                                                                                              Nature 393:537-544(1998).
EMBL; AL021646; CAA16624.1; -.
                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                      InterPro; IPR002989;
InterPro; IPR000030;
                                                                                                                                                                                                                                                                                                                                                         fubercuList; Rv3159c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 DSSVMVRQVGFGNNATANQY
351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GNTAMIIQKGSGNKANITQY
                                             26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQGAY 59
                                                WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
FGNSGNNNIGFENSG-NNNVGFENSGNNNFGFGNAGD
                                                                                                                                                                                                                                                   PF01469; Pentapeptide_
PF00823; PPE; 1.
                                                                                                Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9447 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                     56585 MW;
                                                                                                                                                                                                                                                                                                        PPE.
                                                                                                                                                                                                                                                                                                                              Mycobact_pentapep
                                                                                                                        13.6%;
29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                     Score 105; DB Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 105.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E0C6FB91308CCBDD CRC64;
                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                     9AFC7F02FAEBD588 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                  46;
  -- INTGEGNAGDTNTGE
                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91;
                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
  40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲.
                                                                                                     6
```

ŧ.

Best

```
Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
                                                                                                                                                                                         밁
                                                                                                                                                                                                           δõ
                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                     093397;
093397;
01-NOV-1998
01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                   Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  033801
                              Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-98053981; PubMed=9393832; MEDLINE-98053981; PubMed=9393832; Forentz R.G., Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       033801;
SEQUENCE FROM N.A.
                    NCBI_TaxID=7962;
                                                                           HYOSOPHORIN
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                cells.";
                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression of thin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGFB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                       Infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  738
                                                                                                                                                                                         163
                                                                                                                                                                                                            124
                                                                                                                                                                                                                                  110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 27.0 hes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                        76
                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                      AVVVQKQSHMAIRVTQ 178
                                                                                                                                                                                                            ALVNQTASDSSVMVRQ 139
                                                                                                                                                                                                                                  GNSAAI---
                                                                                                                                                                                                                                                       GNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV------GQYGGNNA 123
                                                                                                                                                                                                                                                                             GSKLLSVISQ-ERGGNNRAKVDQAGNYNFAYIEQTGNAN-----
                                                                                                                                                                                                                                                                                                 GSALAGYVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTGGNGGAGGEVSVSLTDSAIRTGQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQYGGNNAA - - LVNQTASDSSVMVRQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITQSGYGNGADVG------QGADNSTI--ELTQNGFRNNATIDQWNAK---NSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIATAGAGAVGILAQSIGGGGGN---GGNATGGDAGFGSFQIGGGGGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
                                                                                                                                                                                                                                                                                                                                                                            AJ000514;
                                                                                                                                                                                                                                                                                                                        1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      Immun. 65:5320-5325(1997)!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GGYANTANVGFKGLTLTTQGSHAAGIVAQSVGGGGGTGGTASSYSAGIGFTASVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (TrEMBLrel.
3 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                  179 AA;
                                                                                    (TremBLrel. 08, Created)
(TremBLrel. 08, Last seq
(TremBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              CAA04150.1; -.
AA; 19318 MW;
                                                                                                                                                                                                                                  SAAIIQKGSGNKANITQYGTQKTAVVVQKQSHMAIQANITQYGTQKT 162
                                                                                                                                                                                                                                                                                                                                 14.1%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                            aggregative fimbriae promotes interaction um SR-11 with mouse small intestinal epithe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma
                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                 Score 109; DB Pred. No. 0.58;
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                 A2BCCB648B3C0B0B CRC64;
                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      821
                                                                                                                                                                                                                                                                                                                                                                                                                                            J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                 348 AA
                                                     Vertebrata;
                                           Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bian
                                                                                                                                                                                                                                                                                                                                          2;
                                                                                     update)
                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                          Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                            2.,
                                                                                                                                                                                                                                                                             -----DASISQSAY 109
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfeifer
                                           Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                          epithelial
                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                       4;
```

```
RESULT
Q94821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
В
                      δÃ
                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRT RAX
                                               Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                              CONFLICT
SEQUENCE
1640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              094821; p92146; p92145; p92144; p92143; p92142; p92141; 01-FEB-1997 (TEMBLrel. 02, Created) 01-FEB-1997 (TEMBLrel. 02, Last sequence update) 01-DEC-2001 (TIEMBLIel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsao C.C., Huang F.L., Chang Y.S.;
"Purification, characterization, and hyosophorin.";
Mol. Reprod. Dev. 52:288-296(1999).
EMBL; AF077819; AAC27329.1; -
SEQUENCE 348 AA; 33164 MW; 4CEAE1
                                                                                                                                                                                             Nucleic Acids Res. 21:4610-4
EMBL; X06462; CAB37323.1; -.
EMBL; L03710; AAC37171.1; -.
HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                 "Retroviral-type zinc fingers and glycine-rich repeats in encoded by cnjB, a Tetrahymena gene active during meiosis Nucleic Acids Res. 21:4610-4614(1993).
                                                                                                                                                                                                                                                                                                                                 "Multiple introns thermophila.";
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Tetrahymenina; Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetrahymena thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNJB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q94821
                                                                                                                       Zinc-finger.
CONFLICT
                                                                                                                                                 SMART;
                                                                                                                                                           PRINTS;
                                                                                                                                                                      Pfam; PF00098; zf-CCHC;
                                                                                                                                                                                                                                                                      Taylor F.M., Martindale D.W.;
                                                                                                                                                                                                                                                                                   MEDLINE=94051569; PubMed=8233798;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99140211; PubMed=10206660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=OVARY;
                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSALAGVVPQWGGGGNH-----NGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI
QFGGGGNSNGGQSWGTSSGSDWN---
                      {\tt QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TODDGSGSNGTTTQDDGSGSNATTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNQTASDSS-VMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQDDGSGSNATTTQDDGSGSNATTTQDDGSGSNATTTQDDGSGSNATT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TQ-SGYGNGA----DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGSNGTMTQDDGSGSNATTTRDDGSGSNGTTTR----DDGSGSNGTTTQDDGSGSNATT
                                                                                                                                             SM00343; ZnF_C2HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                               39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                           PR00939; C2HCZNFINGER.
                                                                                                                                                                                   IPR001878; Znf_CCHC
                                                                                               251
256
1748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            in a conjugation-specific
                                                                                               251 M -
256 I -
199624 MW;
                                                                                                                                                                                                                                                                                                                     16:2189-2201(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.0%;
27.4%;
                                                          14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                Ciliophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                20;
                                             Score 108; DB Pred. No. 8.5; Nismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 108.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                              -> I (IN REF. 1).
-> N (IN REF. 1).
; 0B03F210104008A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4CEAE146AB760035 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Oligohymenophorea; Hymenostomatida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1748 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3;
 -CQSNVQES-TTTSSGGWGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                       5;
                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72;
                                                29;
                                                                       Length 1748;
                                                                                                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                               Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carp
                                                                                                                                                                                                                                                  ່= ໝ
                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
```

В

121

```
SO DE RECEPTOR OF THE PROPERTY OF THE PROPERTY
                                                                                                                                      SO SET THE REPORT OF THE REPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
Q54069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
   Query Match
Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q93U24
Q93U24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q54069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uhlich G.A., Keen J.E., Elder R.O.; which with Variations in the cspD Promoter Associated with Variations expression in Certain Strains of Escherichia coli 0157:H7." Appl. Environ. Microbiol. 67:2367-2370(2001). EMBL. AF275733, AAK53212.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-43895 RED VARIANT;
MEDLINE-21218556; PubMed-11319125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 EMBL; U53207; AAA98671.1; -
                                                                                                                                                                                                                                                               Cox J.M., Eglezos S., Woolcock J.B.; "Virulence of Salmonella enteritidis in chickens correlates colony morphology and expression of SEF17 fimbriae."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SE30
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEF17 FIMBRIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ນ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
      Local Similarity 98.7 nes 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNNAALVNQTASDSSVMVRQVGFGNNATANQY
| | | | :||||:|| | | ||||||||:||
GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKDSHMTVKQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAATAATVFSGSALAGVVPQYGGGGGHGGGGNNSGPNSELNTYQYGGGNSALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                      76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                      7704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.0%;
                                        49.8%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 564.5;
Pred. No. 2e-
      Pred. No. 1.30); Mismatches
                                        Score 385; DB 2;
Pred. No. 1.3e-21;
                                                                                                                                         2FD5411241A7BCB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
          Indels
                                                                             76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Curli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
          0
```

```
Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                             RESULT 5
Q92UU8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Pı
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TremBLrel.
01-MAR-2001 (TremBLrel.
CURLIN SUBUNIT MONOMER
                                                                                                                                                                                                                            092008:
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL GLYCINE-RICH PROTEIN SMB21548.
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; A
                                                                                                                                                                                                                                                                                                                                                                                                                                               La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078:K80 isolates associated with
"Inserti on in csgB and reduced persistence in poultry infection."
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9S3J5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9S3J5
                                                                                                                                                                                 Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria: Proteobacteria; alpha subdivision:
                                                                                                                                                                                                                                                                                    Q92UU8
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99314153; PubMed=10386375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                    MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester
Vorhoelter F.J., Hernandez-Lucas I., Becker
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPOSON-INSERTION SEQUENCE IS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                      SEQUENCE
                                        "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium mediloti."; proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                                STRAIN=102
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=382;
                                                                                                                                                                         Rhizobiaceae;
                                                                                                                                                                                                                    SMB21548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                          سر
                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IELTQNGFRNNATIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                         MKLLKVAAIAAIVFSGSALAGVVPQYGGG
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                      Hypothetical 2174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                             29 AA; 2789 MW;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                          Sinorhizobium
                                                                                                                                                                                                                                                                                                                                                                                             15.8%;
                     l protein; Complete
203314 MW; 008EB68

    13, Created)
    13, Last sequence (1)
    16, Last annotation R (FRAGMENT).

   14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
  . 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                             Score 122;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                             E290DFC07ABBB243
  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                    subdivision;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation
                      pmplete proteome.
008EB68297B44182 CRC64;
                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                      2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                               .0087;
                                                                                                                                                                                                                                                                                                                                                                                                        BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŗ
  DΒ
                                                                                                                                                                                                                                                                                     AΑ
                                                                                               » □
                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae;
                                                                                                                                                                                    Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                Chain
Cowie
                                                                                                                                                                                                                                                                                                                                                                                                        Length 29;
 Length 2174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      poultry infection.";
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                              P.,
                                                                            from
                                                                                                Gouzy J.,
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                             Z.
                                                                                                                                                                                                                                                                                                                                                                                    0
```

j.

Copyright

GenCore version (c) 1993 - 2002

5.1.3 Compugen Ltd

```
Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
                                                                                                                                                                                                                                                            Post-processing:
                                                                                                                                                                                                                                                                                                                         Total number
                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                      Maximum
                                                                                                                                                                                                                                                                                               Minimum
                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on:
                                                                                                                                                                                                                                                                                  DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                   length:
                                                                                                                                                                      SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-543-407-5
773
                                                                                                                                                                                                                                                                                                                                                                                                                                                          October 11, 2002, 21:05:23; Search time 27 Seconds (without alignments) 967.490 Million cell updates/sec
6:
7:
8:
9:
110:
112:
114:
115:
116:
                                                                                                                                                                                                                                                                                                                                                562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                             MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                  sp_archea:*
sp_bacteria:*
                                                                                               sp_phage:*
                                                                                                            sp_organelle:*
                                                                                                                       sp_mhc:*
                                                                                                                                     sp_mammal:*
                                                                                                                                              sp_invertebrate:*
                                                                                                                                                           sp_human:*
         sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                          sp_rodent:*
sp_virus:*
sp_archeap:*
                                               sp_vertebrate:*
                                                                                    sp_plant:*
                                                                                                                                                                                                                                                                                   2000000000
                                                                                                                                                                                                                                                                                                                         562222
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

104.5 13.5 582 16 P71868 103 13.3 1618 2 Q9KKB1 102 13.2 573 10 Q9SAF2 0	104.5 13.5 582 16 P71868	104.5 13.5 582 16 P71868	TOO 13.0 090 TO 033309	105 13 6 500 16 053300	105.5 13.6 91 2 Q9S3J8 C	13.9 645 16 053818	14.0 1748 5 Q94821 (	14.0 348 13 093397	14.1 179 2 033801 (	14.6 2174 16 Q92UU8	15.8 29 2 Q9S3J5 (	49.8 76 2 Q54069	73.0 152 2 Q93U24	98.8 152 2 033802	No. Score Match Length DB ID Des	•
0981n6 rhizobium 1	Q9saf2 arabidopsis	Q9kkb1 rickettsia	P71868 mycobacteri	O53309 mycobacteri	Q9s3j8 escherichia	O53818 mycobacteri	Q94821 tetrahymena	093397 cyprinus ca	O33801 salmonella	Q92uu8 rhizobium m	Q9s3j5 escherichia	Q54069 salmonella	Q93u24 escherichia	033802 salmonella	Description	

40	- #	<i>\</i>	43	42	41	40	39	38	37	36	<u>3</u> 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
92	) N	٥	92	92	2	92.5	93	93	Ü	93.5	Ü.	94	94	94	ū	95.5	٠	96		96.5			•					99	99.5
11.9	11.	110	11.9	11.9	12.0	12.0	12.0	12.0	12.1	12.1	12.1	12.2	12.2	12.2	12.4	12.4	12.4	12.4	12.5	12.5	12.6	12.7	12.7	12.7	12.7	12.7	12.7	12.8	12.9
. 1440	1400	1227	806	409	1616	629	638	586	1614	447	287	2035	892	652	1613	1306	1053	354	739	319	738	1028	850	615,	552	453	453	764	1615
4	- 4																	16											
CAHCOO	090271	095271	09VBC4	Q19414	Q9KKA5	Q90WR5	Q9XYD8	Q9NAJ4	Q9KKB6	Q9SIA8	Q9VIX6	Q9XCJ4	Q9KX38	Q92G62	Q9KKB2	Q93N36	065937	P95248	Q9X687	Q41725	002402	Q9W4F1	Q9W4F0	P95249	P96840	Q9NGF6	Q9NGF7	Q9BIT1	Q9KKA8
. Матедо пошо зартеп		) I	09vbc4 drosophila	Q19414 caenorhabdi	Q9kka5 rickettsia		Q9xyd8 hirudo medi		Q9kkb6 astrakhan r	Q9sia8 arabidopsis	Q9vix6 drosophila		Q9kx38 moraxella c	2 ricket	μ.	7	7	8	almone]	S		Q9w4f1 drosophila	Q9w4f0 drosophila .	P95249 mycobacteri	P96840 mycobacteri	Q9ngf6 drosophila	Q9ngf7 drosophila	Q9bit1 plectreurys	Q9kka8 rickettsia

## ALIGNMENTS

```
RESULT 1
033802
ID 03380
ρ
                         DЬ
                                                QY
                                                                                Ър
                                                                                                         δÃ
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 149; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        O33802;

O1-JAN-1998 (TrEMBLrel. 05,

O1-JAN-1998 (TrEMBLrel. 05,

O1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-98053981; PubMed-9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes
                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   033802
                                                                                                                                                                                           Infect. Immun. 65:5320-5325(1997).
EMBL; AJO00514; CAA04151.1; -.
NON_TER 152 152
SEQUENCE 152 AA; 15401 MW; 9DA
                                                                                                                                                                                                                                                             "Expression of thin, aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AGFA PROTEIN
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=602;
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                  _
                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                  98.8%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                  Score 764; DB 2;
Pred. No. 4.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                            9DA7DADC2364B006 CRC64;
                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 AA
                                                                                                                                                               Length 152;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                        Pfeifer J.D.,
                                                                                                                                     0,
                                                                                                                                    Gaps
                                                                                60
                                                                                                           60
                                                                                                                                     0;
```

```
밁
                                                                                                                                         ş
                                                                                                                                                                                       ğ
                                                                                                                                                                                                                                ş
Search completed: October 11, 2002, 21:13:42 Job time: 13 secs
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87283911; PubMed=3302276;
Riede I., Drexler K., Eschbach M.L., Henning U.;
Riede I., Drexler K., Eschbach M.L., Henning U.;
"DNA sequence of genes 38 encoding a receptor-recognizing protein of bacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
-I-FUNCTION: VG38 IS AT THE TIP OF THE LONG TAIL FIBERS AND SERVES AS THE PHAGE RECOGNITION SITE FOR THE CELLULAR RECEPTOR.
-I-MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         EMBL; X05312; CAA28935.1; -.
PIR; S00275; S00275.
Fiber protein; Phage recognition.
SEQUENCE 262 AA; 25801 MW; 0567366918F6C745 CRC64;
                                                                                                                                                                                       175 GGGGRPFGVGGKIGSDSILS----GSNASL---TDAGTGGTTF-QYGAGNGGNVGAGGG 225
                                                                                                226 -----RGWGKNVYTSEGGAAGAAVT 245
                                                                                                                                                                                                                 27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD 86
                                                                                                                                           87 NSTIELTQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AS RECEPTORS.
                                                                                                                                                                                                                                                                         11.6%; Score 89.5; DB 1; ilarity 34.1%; Pred. No. 1.9; Conservative 8; Mismatches 33;
                                                                                                                                                                                                                                                                                       33; Indels 17;
                                                                                                                                                                                                                                                                                                                                Length 262;
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                       4
```

institutions as

long

as its content

ıs

in

no

way

Usage

bУ

and

tor

commercial

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 35
"The rickettsial outer membrane protein A and B genes of Ricke australis, the most divergent rickettsia of the spotted fever Submitted (MAY-1999) to the EMBLYGENEARY, DDBJ databases.
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
                                                                                                                                                                                                                                                                                                                                                                      OMPB_RICCN STANDARD; PRT; 1655 AA.

Q9KKA3; Q9KK98; Q9XC45;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide
OMPB OR RC1085.
                                                                  SEQUENCE OF 353-1655 FROM N.A. STRAIN=Malish 7;
                                                                                                                                                     STRAIN-Indian tick typhus, and Malish MEDLINE-20393643; PubMed-10939649;
                                                                                                                                                                                                                             Samson D., Roux V.,
Raoult D.;
                                       "The rickettsial outer membrane
                                                      Stenos
                                                                                                   "Phylogenetic analysis of members of the genus Rickettsia gene coding the outer-membrane protein rOmpB (ompB)."; int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                               SEQUENCE OF 33-1649 FROM N.A.
                                                                                                                                                                                                           Science
                                                                                                                                                                                                                                                                      MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                       Rickettsiaceae; Rickettsieae; NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RICCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                        "Mechanisms of evolution in Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit modified and this st entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Transport; Repeat; CONFLICT 281 282 NA -> (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASTTGGLFGNNGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELTQNG - - FRNNATIDQ - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNNNATANSTGSTGLFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSTTQNGGLFGKPTTTPAGAGGLFGNSSSTNSTTGLFGSNN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S0003060; NUP145.
                                                     J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z32672; CAA83584.1; -. Z72614; CAA96798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X76557; CAA54057.1; -.
                                                                                ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an
                                                                                                                                                                                                                                                                                     FROM N.A.
alish 7;
                                                                                                                                            Raoult D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FGNNATA
                                                      Walker D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281
1142
1310
1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nd this statement is not removed. equires a license agreement (See email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1142
1317
                                                                                                                                                                                                                                             Renesto-Audiffren
Cossart P., Weisse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145660 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GSNNIASSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                    Rickettsia, conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NA -> QR (IN REF. L -> S (IN REF. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L -> S (IN REF. 2).
LMKCTYKI -> FEVYI (IN REF.
                                                                                                                                                                                                                                         iffren P., Fournier P.-E.,
Weissenbach J., Claverie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59399D86BB553030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92.5;
No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB.
                                                                                                                                                                                                                                                                                                                                               Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1317;
                                                                                                                                                                                                                                                        P.-E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                    ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -TQSSTGIFGQKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGGLEGNSNNNNI 146
                                      of Rickettsia
                                                                                                                                                                                                                   prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2).
                                                                                                                                                                                                                                          J.-M.,
                                                                                                                            using
                                                                                                                                                                                                                                                      Barbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                  peptide]
                                                                                                                                                                                                                                                                                                                                                                                              protein
                       group.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
```

```
RESULT
VG38_BI
                                                                                                                                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                            Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SET TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO THE TOTAL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                01-AUG-1988
01-AUG-1988
01-AUG-1990
                                                                                                                                                                                                                             VG38_BPT2
P07875;
                                                                                                                                                                                                                                                                           LT 15
_BPT2
SEQUENCE FROM N.A
                                                           T4-like phages
                                                                                 Bacteriophage
Viruses; dsDNP
                                                                                                                                              Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE008659; AAL03623.1;
EMBL; AF123721; AAF34124.1;
EMBL; AF123726; AAF34129.1;
EMBL; AF149110; AAD39533.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen;
                                                                                                                                                                                                                                                                                                                                                             605
                                                                                                                                                                                                                                                                                                                                                                                                                                                548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490
                                                                                                                                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVER LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY SIMILARITY).
FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ-----SDARKSE
                                                                                                                                                                                                                                                                                                                                                        NAQTLTINGKIGTVGANNKTLGQFNIGSSKTVLSDGDVAINELVIGNN
                                                                                                                                                                                                                                                                                                                                                                                             NAKNSDIT--VGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LADGTVINGKVNQTALVGGALAAGTITLDGSATITGDIGNAGGAAALQGITLANDATK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTITQSGY----GNGADVGQGADNSTIELTQNGFRNNATID------
                                                                                                                                                                                                                                                                                                                                                                                                                                       -TLTLGGANIIGANGGTINFQANGGTIKLTST--QNNIVVDFDLAIATDQTGVVDASSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity 25.0
                                                                                 dsDNA
                                                                                                                                            recognizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s-layer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
413
959
988
1139
353
776
1159
1177
1492
                                                                                                                                                                (Rel.
(Rel.
                                                                                 viruses,
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,
                                                                                                                                                         . 08, Created)
. 08, Last sequ.
. 15, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
413
959
988
1139
176
776
1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1334
1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell wall;
                                                                                                                                        , Last sequence up, Last annotation protein (Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%;
25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168342
                                                                                 no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LI, Complete proteome.

120 KDA SURFACE-EXPOSED PROTEIN.

120 KDA BETA PEPTIDE.

P > A (IN STRAIN INDIAN TICK TYPHUS).

G -> S (IN STRAIN INDIAN TICK TYPHUS).

K -> N (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

V -> D (IN STRAIN INDIAN TICK TYPHUS).

I -> V (IN STRAIN INDIAN TICK TYPHUS).

I -> V (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

B -> D (IN REF. 3).

E -> D (IN REF. 3).

E -> D (IN REF. 3).

E -> C (IN REF. 3).

F -> S (IN REF. 3).
                                                                            RNA stage; Caudovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92;
Pred. No.
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           > R (IN REF. 3).
E49E19377D5FCE37 CRC64;
                                                                                                                                        update)
on update)
in Gp38).
                                                                                                                                                                                                                                                   262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
3.6;
                                                                                                                                                                                                                                                 AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                            Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COVERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŷ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ву а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
```

SQ DR

```
ICEA_PANAN

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Best [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00818; Ice_nucleation; 65. PRINTS; PR00327; ICENUCLEATN. PROSITE; PS00314; ICE_NUCLEATION; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICEA_PANAN
P20469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M26382; AAA24823.1;
PIR; JQ0188; JQ0188.
HSSP; P06620; IINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequal 16-OCT-2001 (Rel. 40, Last annotations)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
"An ice nucleation active gene of Erwinia ananas. Sequence similarity
to those of Pseudomonas species and regions required for ice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleation activity.";
FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pantoea ananas (Erwinia uredovora)
                                                                                                                                                    between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90092494; PubMed-2599095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VAAFAAIVVSG---SALAGV-VPQWGGGGNH----NGGGNSSGPDSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleation; Repeat; Outer membrane.
                                                                                                                                                                                                                                                                                                  CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS
OCTAPERTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: ICE NUCLEATION PROTEINS
                                                                                                                                                                                                                                                                             FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAGYGSTQTAGEESSQMAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSL-IAGYGSTQTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGSTQTAQK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGNNATANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALQSDARKSETTITQSGYGN-----GADV-----GQGADNSTI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQTAGYGSTQTAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQN-GFRNNATIDQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVG
                                                                                                                                                                                                                   SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000258; Ice_nucleatn 0818: Ice_nucleation; 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·GEDSSLTAGYGSTQTAQKGSDLTAGYGSTGTAGADSSLIAGYGSTQTAGEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.4%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .7 OCTAPEPTIDE PERIODICITY 125084 MW; 590E8A130077FBD4 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGSDLTAG-YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1322
                                                                                                                                                                                                                   It is produced through a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENABLE BACTERIA TO
                                                                                                                            There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arai S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                        and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
                                                                                                                                                                                                                       collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ė
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                     9
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
```

```
NIAS_TESULT 13
NIAS_Y
NIAS_TESULT
NIAS_Y
AC P49687
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FCB
CC P49687
AC P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR DR DR DR DR DR DR DR FT SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996
01-FEB-1996
01-NOV-1997
                                                                                                                                                                                                                          Rieger M., Brueckner M., Schaefer M., Mus
"Sequence analysis of 203 kilobases from
chromosome VII.";
Yeast 13:1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X17316; CAA351
PIR; S07053; S07053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleoporin NUP145 (Nuclear pore NUP145 OR YGL092W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1014 SSQTARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ice nucleation; Repeat; Outer membrane DOMAIN 162 1281 OCTAPEPTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000258; Ice_nucleatn
Pfam; PF00818; Ice_nucleation; 69
  between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94320139; PubMed=8044840;
Fabre E., Boelens W.C., Wimmer C., Mattaj I.W., Hurt
"Nupl45p is required for nuclear export of mRNA and b
homopolymeric RNA in vitro via a novel conserved moti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P49687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N145_YEAST
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                               "NUP145 encodes a novel yeast glycine-leucine-phenylalanine-glycine (GLFG) nucleoporin required for nuclear envelope structure.";
J. Cell Biol. 125:955-969(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homopolymeric RNA in v
Cell 78:275-289(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=94320139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       933
                                                                                                                                                                                                                       Yeast
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wente S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94253246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 NNATANO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                           DOMAIN: CONTAINS G-L-F-G REPEATS.
                                                                                                                                                                St 13:1077-1090(1997).

FUNCTION: MAY PLAY A DIRECT ROLE IN NUCLEOCYTOPLASMIC EXPORT RNA AND ALSO IN PROTEIN IMPORT. BINDS HOMOPOLYMERIC RNA.
                                                                                                    SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
  European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNGFRNNATIDQWNAKNSDITVGQYG-----GNNAALV----NQTASDSSVMVRQVGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSTSTAGPDSSL-IAGYGSTQTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P06620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 13
1322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 35, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blobel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINA
       Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA35194.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / x2180;
PubMed=8195299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QENSDLTTG-YGSTSTAGYESSLIAGYGSTQTASFKSTLM--AGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1%; 28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131094 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
       Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89B0EE24AA837039 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GYNSILTAGYGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                       Mueller-Auer S.; rom Saccharomyces
                                                                                                                                                    complex.
  There are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUP145).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and binds motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
       ö
          restrictions
                                                                                                                                                                                                                                                                            cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            967
          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
••
```

STINE DE REPRESENTATION DE LA COCCACA COCCACA

EMBL outstation

no 9

```
RESULT 10
ICEN_PANAN
ID ICEN_PANAN
ID ICEN_PANAN
ID ICEN_PANAN
ID ICEN_PANAN
ID ICEN_PANAN
ID ICEN_ICEN
INAU.
OS PANTOE
OC PANTOE
OC PANTOE
OX MEDLLY
RN MICHI_T
RN [1]
RP SEQUEN
RC MICHI_T
RN MICHI_T
CCC -!- SI
CCC -!- MI
CCC -!- MI
CCC -!- SI
CCC -!- S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 215035; CAA78753.1; -.
EMBL; X75780; CAA53406.1; -.
EMBL; Z8068; CAA61905.1; -.
PIR; B44402; B44402.
PIR; S39173; S39173.
PIR; S44518; S44518.
SGD; S0001551; NUP100.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          047879;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                             Biosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uredovora.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94264407; PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H., Ar "Cloning and sequencing of an ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-KUIN-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pantoea ananas (Erwinia uredovora)
Bacteria; Proteobacteria; gamma su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICEN_PANAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03093; Nucleoporin_FG; 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004325; Nucleoporin_FG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                   FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUC
CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: Outer membrane.
SUBCELLULAR LOCATION: Outer membrane.
DOMAIN: CONTAINS IMPEREDENT REPEATS OF A CONSENSUS OCTAPE
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL
PERIODICITY IS SUPERIMPOSED.
MISCELLANGEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT O
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFGSKPVGSGSLFGQSNNTLGNTTN--NRNGLFGQMNSSNQ------GSSNSGLFGQNS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGNHNGGGNSSGPDSTLSIY--QYGSANAALALQSDARKSETTITQSGYGN-----GA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNSST --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVGQ-----GADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNOTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNGSNIFGAGNNSQSNTTGSLFGNQQSSAFGTNNQQGSLFGQQSQNTNNAFGNQNQLGGS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotechnol. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -QGVFGQN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \frac{\omega}{\omega}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transport; Repeat.
571 29 x 6 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99988 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; 27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      58:762-764(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-L-F-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D3985F9901BBAA51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 959
2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                      WHICH THE
                                                                                                                                                                                                                                                                                                                OCTAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엵
                                                                                                                                                                                                                                                                                48-RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
```

Вþ Ş Ъ ο<sub>γ</sub> ₽ οy

```
RESGULT 11
ICEN_EMMHE
ID ICEN_E
AC P16239
DT 01-APR
DT 01-APR
DT 16-OCT
DE ICE ICE
OC PANTO
OC I-- FU
OC I-- SI

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
  This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                       CRYSTALLIZATION IN SUPERCOOLED WATER.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS 126 IMPERFECT REPEATS OF A C
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seg
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      herbicola, Pseudomonas fluorescens and Gene 85:239-242(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Warren G.J., Corotto L.V.;
"The consensus sequence of ice nucleation proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90152370; PubMed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P16239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00327; ICENUCLEATN. PROSITE; PS00314; ICE_NUCLEAT
                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pantoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ice nucleation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICEN_ERWHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 993 OCTAPEPTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D14992; BAA03636.1; -. . . HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 YGSTQTAQK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                        PERIODICITY IS SUPERIMPOSED.

MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED NUCLEATION PROTEIN DISPARYS A SYMMETRY RELATED SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAFAAIVVSG----SALAGV-VPQWGGGGNH----NGGGNSSGPDSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TQTAGYGSTQTAQ - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAGYGSTQTAGEESSQMAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSL-IAGYGSTQTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQN-GFRNNATIDQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALQSDARKSETTITQSGYGN-----GADV------GQGADNSTI------EL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1034 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEDSSLTAGYGSTQTAQKGSDLTAGYGSTGTAGADSSLIAGYGSTQTAGEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICE_NUCLEATION; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.4%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103378 MW; FA222523D333EADD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGSDLTAG-YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 95.5; D
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision;
                                                                                   It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AΑ
                                                                                                                                                                                           ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                            CONSENSUS OCTAPEPTIDE
                                                                                                                                                                                                                                                                                                A REGIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                 IN WHICH THE ICE TO THAT OF ICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            syringae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                  48-RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266
```

There are no restrictions ng as its content is in

and the

EMBL

outstation

, 1

9

its

Usage

and

for

commercia.

```
THE SULTY YEAR OLD DIT IN THE SULTY YEAR OLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                    Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C., III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv1548c.
RV1548C OR MT1599 OR MTCY48.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YF48_MYCTU
Q10778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996
                                                                        This
                                                                                                                                                                                                                          Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales;
                                                   between
                                                                                                               laboratory strains.";
Submitted (APR-2001) to
-|- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 NNNN----NNNGGQTSMMGHPF-YGGNPSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                   Whole genome comparison of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
      European Bioinformatics Institute. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI----TVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGNNAALVNOTASDSSVMVROVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQNAAAAAYIMSAGSG-----
                                              SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                               FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  797
820
826
874
874
874
902
930
930
947
1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGNGYINCGGVG-GPNNS---LDGNNLLNFASVSNYNESNSKFHNHHHHHQH
                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34, Created)
38, Last sequence up
40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         802
823
832
992
896
896
896
953
953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110620
                                                                                                                  the EMBL/GenBank/DDBJ databases TO THE MYCOBACTERIAL PPE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLN.
ZINC FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2H2-TYPE.
A -> R (IN REF. 2).
M; D7068BB2BC0F6F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·GGGCTGNGGGGASGPGGGPSANSGGGGGGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.5;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            678
                           There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1028;
             restrictions tent is in
                                                                                                                                                                                          clinical and
                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harris
                                                                            collaboration
                                                                                                                                                                                                                                                                                Ħ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                    S.L.,
A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
             no
on
```

```
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE007026; AAK45866.1; TIGR; MT1599;
                                                                                                                                                                                                                                                                                                                                                                                002629;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Nucleoporin NUP100/NSP100 (Nuclear pore protein
NUP100 OR NSP100 OR YKL336
                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; 'TRANSMEM 14 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rubercuList; Rv1548c;
                                                           "Sequence of a 20.7 kb region of yeast chromosome XI includes the "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUPIOD gene, an open reading frame (ORF) possibly representing a nucleoside diphosphate kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to known proteins.",

Yeast 10:S69-S74(1994).

Yeast 10:S69-S74(1994).

Yeast 10:S69-S74(1994).

THE PROTEINS MAY BE INVOLVED IN BOTH BINDING AND TRANSLOCATION THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
                                                                                                                                                                                                                                               MEDLINE-93054906; PubMed-1385442; Wente S.R., Rout M.P., Blobel G.; Wente S.R. will yof yeast nuclear pore J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N100_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002989; Mycobact_pentapep
InterPro; IPR000030; PPE;
                                                                                                                                                                                                MEDLINE-94378724;
                                                                                                                                                                                                            STRAIN-S288C
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
 This
                                                                                                                                                                                  Rasmussen
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 HNIGFGNSGNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                   SUBCELLULAR LOCATION: Nuclear pore complex.
DOMAIN: CONTAINS G-L-F-G REPEATS.
SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROVGEGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGGG--GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGGGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGADNSTIELTON---GFRNNATIDOWNAKNSDITV--GQYGGNNAALVNQTASDSSVMV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGSGNIGSYNLGGGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00823; PPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01469; Pentapeptide_2; 13.
 SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                  S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAA98335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TGNSNFGFGNTGNVNFGNGNTGDTNFGSGNLGSGNIGFGNKGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
 entry is
                                                                                                                                                                                                PubMed=8091863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
258
66736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
 copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LGSYNLGSGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
D -> G (IN REF. 2).
; 209F1593D52533A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
 Ιt
                                                                                                                                                                                                                                                                 complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
1.1;
 is produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Usage by and for http://www.isb-sib.
                                                                                                                                                                                                                                                                 proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 678
                                                                                                                                                                                                                                                                                                                                                                                                 NUP100/NSP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGDTNFGGGNTGNLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
    through a
                                                                                 TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ch/announce/
     collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

of Drosophila

```
RESULT 7
OVO_DROME
                                                                                                                                                           δÃ
                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
       DAC
DT
                                                                                                                             Ъ
                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                        Matches
OVO_DROME STANDARD;
P51521; Q9XZU4;
01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICEMUCLEATIN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990
01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICEN_XANCT
P18127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P06620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X52970; CAA37140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-X56S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91080859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Conserved repetition in the ice nucleation gene inax
                                                                                                                            318
                                                                                                                                                              104
                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: OUTES membrane (By similarity).
DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE IC
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                             nucleation;
UENCE 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gen. Genet. 223:163-166(1990).
FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleation
                                                                                                                                                                                                                                                                                                   VSGSALAG-----VVPQWGG----GGNHN------GGGNSSGPDSTLSIYQYGSANAALAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S11672; S11672.
                                                                                                                                                       ---DQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ
                                                                                                                          YGSTQTARKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK
                                                                                                                                                                                             STLTAGYGSTQTAQEGSRLTSGYGSTAT---SGSDSAVI----SGYGSTQTAGSESSLTAG
                                                                                                                                                                                                                                                                    VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orser C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      campestris
                                                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1INA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Outer membrane. AA; 152548 MW; C8B451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                        13.1%; 27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Last
, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (pv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence up
annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translucens).
                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                         Score 101.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                          ö.
                                      1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1567
                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AΑ
                                      AΑ
                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                          53
;
                                                                                                                                                                                                                                                                                                                                                                         Length 1567;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICE
                                                                                                                                                                                                                                                                                                                                        12;
   THE PROPERTY OF THE PROPERTY O
 DOMAIN
                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00028; ZINC_FINGER_C2H2_1; PROSITE; PS50157; ZINC_FINGER_C2H2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00048; ZINCFINGER. SMART; SM00355; ZnF_C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000822; znf-C2H2.
Pfam; PF00096; zf-C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U11383; AAB60216.1;
EMBL; X59772; CAB36921.1;
HSSP; P25490; 1ZNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene region melanogaster: relationship to genetic complexity."; mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ovo protein (Shaven baby protein).
OVO OR SVB.
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                       Transcription
                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0003028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for female germ line development.";

EMBO J. 10:2259-2266(1991).

-i- FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM

LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-i- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mevel-Ninio M.T.M., Terracol R., Kaf
"The ovo gene of Drosophila encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91293102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95021209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN THE BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      melanogaster (Fruit fly)
 regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1712294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=7935398;
 ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                         DNA-binding;
                                                                   POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-ALA.
                                                                                                                                                                                                              POLY-ASN.
POLY-GLN.
POLY-GLN.
                                                                                                                                                                                                                                                                 POLY-GLY.
                                                                                                                                                           POLY-GLN
                                                                                                                                                                             POLY-GLN
                                                                                                                                                                                             POLY-GLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y., Mahowald A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kafatos F.
des a zinc
                                                                                                                                                                                                                                                                                                                                                                                           ww
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                         Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .C.;
finger protein required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
```

γd

and for

LSALTY CSGB\_SALTY P55226;

STANDARD;

PRT;

151 AA

```
õ
                                         Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
01-OCT-1996
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last Sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.enteritidis; STRAIN=270
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., w Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nha Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-S.typhimurium; STRAIN-SR-MEDLINE-98117058; PubMed-9457880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Romling U., Bian 2., Hammar M., Sierralta W.D., No "Curli fibers are highly conserved between Salmone Escherichia coli with respect to operon structure J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision;
                                                                                                       SEQUENCE
                                                                                                                                                 Fimbria;
                                                                                                                                                               StyGene;
                                                                                                                                                                                EMBL; U43280;
                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collinson S.K., Clouthier S.C., Doran J.L., Banser salmonella enteritidis agfBAC operon encoding thin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome
51 GSANAALALQSDARKSE-----TTITQSGYGNGADVGQ-GADNST------
                                                                                                                                                                                                                                                                                                                                                                                             BACTERIO1. 178:662-667(1996).

FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AND COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: STRONG, TO E.COLI CSGB
                                                                                                                                                                                                                                                                                                                                                                                 CURLIN MONOMERS.
                                                                                                                                                                                               AJ002301; CAA05316.1; -. AE008749; AAL20073.1; -.
                                           l Similarity
36; Conserv
                                                                                                                                    Signal; Complete proteome
1 21 POTEN
                                                                                                                                                                 SG10609; csgB
                                                                                                    1
22
151 AA;
                                            Conservative
                                                                                                                                                                             AAC43598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of Salmonella enterica serovar Typhimurium
                                                                                                                       151
                                                                                                         16182
                                                         14.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SR-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-27655-3B;
                                                                                                         XW:
                                                         Score 111.5;
Pred. No. 0.
                                                                                                      POTENTIAL.
MINOR CURLIN SUBUNIT; C0FC5430E6DD361D C1
                                         Mismatches
                                                            .021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W.D., Normark of Salmonella ty.
                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae,
                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minor subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thin,
                                                                                                         CRC64;
                                                                          Length
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Latreille P., ou S., Layman D., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  typhimurium regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ß
                                                                                                                                                                                                                                                                                                                      a collaboration
              --IELTQ 94
                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ... and
ግ. ";
                                            Gaps
                                              5
```

```
OMPB_RICJA
ID OMPB_R
AC O06653
AC O06653
DT 30-MAY
OC Ricket
OC This S
OC -!- SI
OC -!- SI
OC -!- SI
OC -!- SI
OC OT Se
OC This
OC OT Se
OC O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вþ
Дb
                                         20
                                                                                             Db
                                                                                                                                       δÃ
                                                                                                                                                                                              Вр
                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompB)
(romp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptidel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMPB_RICJA STANDARD; PRT; 16
006653;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uchiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-YH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia japonica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outsi
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequencing of the gene encoding the japonica.";
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003858; rOmpA_1
Pfam; PF02708; rOmpA_rOmpB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB003681; BAA20138.1;
                                                 105
                                                                                                                                                                                                 509
                                                                                                   548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                               66
                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAYER WITH HEXAGONAL SYMMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGGNNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGFRNNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSYMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
LTNAQTLTISGTIGIIGANNTTLGQFNIGSSKTTLNGGNVAINELVIGNNGS
                                                                                                                                                                                                 VLAAGAITLDGSATI-----
                                                                                                                                                                                                                                                  VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK
                                              QWNAKNSDI--TVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT
                                                                                                                                            SETTITQSG----YGNGADVGQGADNSTIELTQNGFRNNATID-----
                                                                                                                                                                                                                                                                                                 l Similarity
45; Conserv
                                                                                                -TLTLGGANIISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQTGVVDASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-layer;
                                                                                                                                                                                                                                                                                                                                                                                                                         1339
528
                                                                                                                                                                                                                                                                                                                                                                                                  1656 AA;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell wall.
1338
                                                                                                                                                                                                                                                                                                                                                                                                                         1656
533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rOmpA_rOmpB.
                                                                                                                                                                                                                                                                                                                      13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                    168097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                   -TGDIGNGGG
                                                                                                                                                                                                                                                                                                                                                                                                    MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲
                                                                                                                                                                                                                                                                                                                         Score 103;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                       120 KDA SURFACE-EXPOSE SOLVER STA PEPTIDE POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WALL.
                                                                                                                                                                                                                                                                                                 ed. No. 1.2;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SURFACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŗ
                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rOmp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsiales;
                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                              Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W
                                                                                                                                                                                                      GAALQSITLANDATK
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \mathbf{s}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COVERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
     654
                                                                                                                                                                                                                                                                                                    56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY A S-
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                      547
                                                                                                                                                                                                                                                     65
                                                                                                                                                       104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           way
                                                                                                                                                                                                                                                                                                    8
```

```
ACCOCC REPORT OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR DR DR DR DR DR FT FT FT SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
                                                                     Mori H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDITARE—96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.,
"Expression of two csg operons is required for product fibronectin- and congo red-binding curli polymers in E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EcoGene; Fimbria;
                                               Sampei G.,
                                                                                                                                                                       MEDLINE=97061202;
                                                                                                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                      Gregor J., Davis N.W.,
                                                                                                                                                                                                                                                                                                                                                          Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECOLI
                                                                                                                       Ikemoto
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D90741;
EMBL; D90742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                B., Shao Y.;
                                                                                                                                                                                                                                                                complete genome sequence nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSYMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAIAAIVESGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG}
                                  T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., O K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE000205; AAC74126.1; -. D90741; BAA35832.1; -. D90742; BAA35840.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                      Horiuchi T.
                                                                                                                                                                                                                 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EG11489; csgA.
Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MC4100;
sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA23616.1;
CAA62282.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83334;
                                                                                                                                                                  PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.8%;
74.8%;
                                                                                                                                                                                                                                                                                                                                    Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 586; DB 1
Pred. No. 2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAJOR CURLIN SUBUNIT.
Escherichia coli K-12
                                                                                                                                                                                                                                                                                       of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> E (IN REF. 1)
C003470D208D395F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     required for production curli polymers in Esch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                    Goeden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                 ., Perna N.T., Burland
Rode C.K., Mayhew G.F
3oeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                       coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

```
Qy
                                      Ъ
                                                                     Ωy
                                                                                                                                                                              Matches
                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arnqvist A., Olsen A., Normark S.;

*Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";

MOL Microbiol. 13:1021-1032(1994).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                   Fimbria;
                                                                                                                                                                                                                                                  EcoGene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95157246; PubMed=7854117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
     86
                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: STRONG, TO SALMONELLA CSGB.
SIMILARITY: TO CURLIN MAJOR SUBUNIT (CSGA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURLIN MONOMERS.
 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                     SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                  X90754; CAA62281.1; -. AE000205; AAC74125.1; -. D90741; BAA35831.1; -. AE005315; AAG55787.1; -.
                                                                                                                                                                                                                                                                AP002554; BAB34842.1; -.
                                                                                                           . Similarity
35; Conser
                                                                                                                                                                                                      GOLDAN, CSGB.
EGIDAGI, CSGB.
Signal; Complete proteome.
POTENTIAL.
                                                                                                                                                                            151 AA;
                                                                                                           Conservative
                                                                                                                                                                              15882
                                                                                                                         14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.A.
                                    AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                                                                            MW;
                                                                                                         13;
                                                                                                                         Score 112.5; DB Pred. No. 0.017;
                                                                                                                                                                                               MINOR CURLIN SUBUNIT.
                                                                                                                                                                           B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700927;
                                                                                                         Mismatches
                                                                                                                                          DB 1;
                                                                                                       61;
                                                                                                       Indels
                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yokoyama K.,
Tobe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration -
                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                       Gaps
                                                                      97
                                    76
                                                                                                       2
```

밁

77

SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY

```
RESULT 2
CSGA_EGA_E
ID CSGA_E
P28307
AC P28307
DT 01-OEC
DT 01-OCT
DT 16-OCT
DT 16-OCT
DT MAJOR
GN CSGA C
OS Escher
                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                              В
                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                    S
                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
or send a
                                                  01-DEC-1992
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. BBCTETIOL. 173:4773-4781(1991).

-:- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-:- COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doran J.L., Collinson S.K., Burian J., Sarlos G., 7 Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., For P.N., Bansed diagnostic tests for Salmonella species the structural gene for thin, aggregative fimbriae J. Clin. Microbiol. 31:2263-2273(1993).
                                                                                     CSGA_ECOLI
P28307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91310586; PubMed=1677357
Collinson S.K., Emoedy L., Muell
                           Major
CSGA (
                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 21-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fimbriae.";
J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94013373; PubMed-8104955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 21-151 FROM N.A.
 Bacteria;
                Escherichia
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                          Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       StyGene;
                                                                                                                                                                121
                                                                                                                                                                                        121
                                                                                                                                                                                                               61
                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRONECTIN.
                                                                                                                                                                NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                       NNAALVNOTASDSSVMVROVGFGNNATANQY
                                                                                                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ002301; CAA05317.1; -. AE008749; AAL20074.1; -. AL627269; CAD08268.1; -. U43280; AAC43599.1; -.
                                        curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       ; Signal; Complete | 1 20 151 151 T 134 151
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        SG10608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enteritidis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .enteritidis;
   Proteobacteria;
                                     (Rel. 34,
(Rel. 40,
n_subunit p
                                                                                                                                                                                                                                                                                                                                                                151
               col1
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178:662-667(1996).
                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRONG, TO E.COLI CSGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emoedy L., Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                         csgA
                                                                                                                                                                                                                                                                                                                                                              15305
                                                                                                                                                                                                                                                                                                                          100.0%;
                                                  Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-27655-3B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-27655-3B,
                                                                                                                                                                                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                           proteome
   gamma
                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                REF. 5).
B7DAC0D16B621359
                                                                                                                                                                                                                                                                                                                                                                                       SVMVRQVGFGNNATANQY ->
                                                                                                                                                                                                                                                                                                                                                                                                    MAJOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                         Score 773;
Pred. No. 5.
                                                                                                    PRT;
   subdivision;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of thin,
                                                             update)
                                                                                                                                                                                        151
                                                                                                   151
                                                                                                    A
                                                                                                                                                                                                                                                                                                               3.2e-54;
3s 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trust T.J.,
                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rust T.J., Kay W.W.;
aggregative fimbriae
   Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Todd E.C.D.,
Kay W.W.;
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          targeting agfA
.";
                                                                                                                                                                                                                                                                                                                                                                                        DSYTQVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GROWTH
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from
                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                0;
```

```
Oshima T., Aiba H., Baba T., Fujita K., Ikemoto K., Inada T., Itoh T., Kajihara Kimura S., Kitagawa M., Makino K., Masuc Mori H., Motomura K., Nakamura Y., Nashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., M. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
                                                                                                                                                                                       J. Bacteriol. 173:4773-4781(1991).
-:- FUNCTION: COTLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. (
-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                    SEQUENCE OF 21-31

MEDLINE=91310586; PubMed=1677357;

COllinson S.K., Emoedy L., Trust T.J., Kay W.W.;

"Purification and characterization of thin, aggregative
                                                                                                                                                                                                                                                                                                                                                 Arnqvist A., Olsen A., Pfeifer J., "The Crl protein activates cryptic fibronectin binding in Escherichia Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sampei G., Seki Y., T
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibronectin- and congo red-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.; "Expression of two csg operons is required for production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96414468; PubMed=8817489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repression of csgA,
Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
STRAIN=K12 / W311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia
             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 21-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97061202; PubMed-8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mau B., Shao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>M</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLINE-93211294; PubMed-8459772;
                                                                                                                                                                                                                                                     Salmonella enteritidis."
                                                                                                                                       FIBRONECTIN.
- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n A., Arnqvist A.;
RpoS sigma factor relieves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microbiol. 7:523-536(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MC4100;
                                                                                                                                   STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18:661-670(1995).
                                                                                                                             CURLIN MINOR SUBUNIT (CSGB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tagami H., Takemoto K., Wada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subunit
                                                                                                                                                         TO
                                                                                                                                                         SALMONELLA CSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ujita K., Hayashi K., Honjo A.,
Kajihara M., Kanai K., Kashinoto K.,
K., Masuda S., Miki T., Mizobuchi K.
Y., Nashimoto H., Nishio Y., Saito N
Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H-NS-mediated transcriptional
gene of fibronectin-binding c
                                                                                                                                                                                                                                                                                                                                                                   Russell D.G., Normark S.; genes for curli formation coli HB101.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rode C.K., Mayhew G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rose
                                                                                                                                                                                                                                                                         fimbriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    curli
                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                          CURLI
                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
```

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ritle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein -
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB seq
   586
1112.55
1111.55
1111.55
1103
1001.59
98.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
99.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
89.55
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-543-407-5
773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 11, 2002, 21:05:23 ; Search time 10 Seconds (without alignments) 584.665 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105224 seqs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALA,......DSSVMVRQVGFGNNATANQY 151
   134.
122.13.
134.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.13.
132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSGB_SALTY
OMPB_RICJA
ICEN_XANCT
OVO_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICEA_PANAN
N145_YEAST
OMPB_RICCN
VG38_BPT2
IMD_ARTGO
MBN_DROME
YM96_YEAST
HYR1_CANAL
Y136_TREPA
ILF3_HUMAN
SGG_DROME
                                                                                                                                                                                                            YBIL_ECOLI
ICEV_PSESX
YKO3_CAEEL
ICEN_PSEFL
ICEN_PSEFL
YKO9_MYCTU
Y442_MYCTU
ICEK_PSESX
NSESX
NSPL_YEAST
MSA2_PLAFZ
PER_DROWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N100_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YF48_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICEN_ERWHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105224
P398307
P39828
P55228
P55228
P10653
P10778
Q10778
Q10778
Q147879
P16239
P16239
P16239
P175780
O33479
P175780
O3349
P175780
O3449
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 pantoea ana
9 erwinia her
9 pantoea ana
7 saccharomyc
                                                                                     saccharomyc
candida alb
                                                                                                                                                    arthrobacte
drosophila
                                                                                                                                                                                                               plasmodium
drosophila
                                                                                                                                                                                                                                                                                                                                                                    mycobacteri
mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                               pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                            pseudomonas
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacteriopha
escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xanthomonas
drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r outer mem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     escherichia
escherichia
                               treponema p
h interleuk
                                                                                                                                                                                                                                                                           saccharomyc
                                                                                                                                                                                                                                                                                                        pseudomonas
                                                                                                                                                                                                                                                                                                                                       pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r outer mem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     saccharomyc
```

45	44	43	42	41	40	39	38	37	36	35	34
. 81	81	81	81.5	81.5	81.5	82.5	83	83	83	83.5	83.5
10.5	10.5	10.5	10.5	10.5	10.5	10.7	10.7	10.7	10.7	10.8	10.8
443	400	165	1063	548	392	369	543	429	342	1156	1113
<u> </u>	ᆫ	٢	۲	$\vdash$	Н	$\vdash$	<del>ب</del>	۲	<del>ب</del>	۳	_
Y878_MYCTU	RTOA_DICDI	GRP1_ORYSA	SPT5_YEAST	CEAK_ECOLI	HME1_HUMAN	PST3_MYCAV	YP91_MYCTU	DR48_YEAST	OMPC_RAHAQ	GLH4_CAEEL	N116_YEAST
Q10540 mycobacteri	P54681 dictyosteli	P25074 oryza sativ	P27692 saccharomyc	Q47502 escherichia			Q50630 mycobacteri			~	Q02630 saccharomyc

### ALIGNMENTS

RP RX RA	R R R R R R R R R R	RA RA	RA RA	RARA	R R	RN	R R F	RA :	RA	R R	RR	P.P.	RAR	7 X C	R R	288	200	80	GN E	DI	DT	RESULT CSGA_S ID C
SEQUENCE FROM N.A. SPECIES-S.enteritidis; STRAIN-27655-3B; MEDLINE-96146512; PubMed-8550497; Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.; "Salmonella enteritidis agfBAC operon encoding thin, aggregative	genome sequenc serovar Typhi ( 3:848-852(2001)	r S., Moule S., O'Gaora P., Parry Conds M., Skelton J., Stevens K.,	Baker S., Basidam D., Blooks R., Chillingworth I., Commercum r., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hlen T.T., Holroyd S., Jagels K.,	ill J., Dougan G., James K.D., Thomson N.R., Pickard D. ill J., Dougan G., James K.D., Thomson N.R., Pickard D. her C., Mungall K.L., Bentley S.D., Holden M.T.G., Seba	SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=CT18;	Nature 413:852-856(2001). [3]	_	han M.,	Hou S., Layman N., Mulvanev E.	Contact   Clifton C W   Tatroille B	UENCE FROM N.A.	J. Bacteriol. 180:722-731(1998).	ella typhimurium	÷	SEQUENCE FROM N.A.	Salmonella. NCBI_TaxID=602, 601, 592;	Salmonella enteritidis. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		OR STY1181.	(Rel. 41,	34, Created)	a la la la